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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 YDRLEQLAGNLRENIELGNGPLEBAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182
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Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.1%; Score 1010; DB 1; Length 267; 100.0%; Pred. No. 1.5e-110;
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                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: O'-JUN-1995
CLASSIFICATION: 530
TITLE OF INVENTION: Immunotoxins Comprising Ri
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESONDENCE ADDRESS:
ADDRESSES: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. NO.
                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 007-007-1995
CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UNN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/91,707
FILING DATE: 19-UNN-1992
RILING DATE: 19-UNN-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: McNicholas, Janet M. REGISTRATION NUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 YIEGEMRTRIRYNRRS 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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amino acid
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                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                        Illinois
: USA
                                                                                                       STREET: Soc
TTTY: Chicago
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                                                                                                                                                                        STATE: Il
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US-08-646-360-1

RESULT 9

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63 SNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYTFAFGGN 122
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                                                                        APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRILIGADATE: 13-MAY-1996
CLASSIFICATION: 530
RIGASSIFICATION DATA:
APPLICATION DATA:
PILING APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1994
RICAR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 05-DEC-1992
RICAR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
RICAR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
RICAR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MONICOPIAS, JADEC M.
REFERENCE/DOCKET NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 32,918
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION PROPERSOR 1248
TELEFAX: 312/707-9155
INFORMATION FOR SEQ 1D NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 1, Application US/08646360 Patent No. 5837491 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 YIEGEMRTRIRYNRRS 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                            ADDA...
STREET: 500 ...
CITY: Chicago
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Best Local Similarity
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US-08-646-360-1
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123 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182
                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09136389

Patent No. 6146850

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrewa, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.1%; Score 1010; DB 3; Length 267; 100.0%; Pred. No. 1.5e-110; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PRILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 04-NOV-1991
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                       183 YIEGEMRTRIRYNRRS 198
                                                                                                                       183 YIEGEMRTRIRYNRRS 198
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amino acid
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Best Local Similarity 100.
Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312/707-9155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
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                                                                                                                                                                                                                         APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 267;
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99.1%; Score 1010; DB 3; L
Best Local Similarity 100.0%; Pred. No. 1.5e-110;
Matches 196; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11022US09/200-70.P3.C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATE:

PRILING DATE:
12-MAY-1993

PRIOR APPLICATION DATE:
PILING DATE:
12-MAY-1993

PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/988,430

FILING DATE:
09-DEC-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707

FILING DATE:
19-UN-1992

PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/787,567

FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME:
REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 11022US09/2

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                            Sequence 1, Application US/08839765
Patent No. 6146631
GENERAL INFORMATION:
                          183 YIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 267 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 196; Conservative
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, MOLECULE TYPE: protein US-08-839-765-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 500 Wee CITY: Chicago STATE: Illinoie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60661
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                                                                                                                            JS-08-839-765-1
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SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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: Illinois
'RY: USA
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                                                                                                                    63 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
                                                                                                                                                                                                                   123 YDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182
                                                   3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 62
                       PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHBIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09610838
Patent No. 6376217
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,838
FILING DATE: 06-UUL-2000
CLASSIFICCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: McAndrews, Held & Malloy, Ltd. STREET: 500 West Madison Street, 34th floor CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRICRA APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
FILING DATE: 18-A02 1996
FILING DATE: 13-MAY-1996
FILING DATE: 13-MAY-1996
FILING DATE: 12-MAY-1994
FILING DATE: 12-MAY-1994
FRICH APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
FRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 19-MAY-1993
FRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 19-UN-1992
FRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
FRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
FRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
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FILING DATE: 04-N0V-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCM.cholas, Janet M.
REGISTRATION NUMBER: 32,918
REPERENCE/DOCKET NUMBER: 200-70.P4
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 1:
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Sequence 1, Application PC/TUS9209487
GENERAL INFORMATION:
APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Line, Julie A.
APPLICANT: Line, Julie A.
APPLICANT: Line, Julie A.
APPLICANT: Line, Shau-Ping
ITILE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122
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                                                                                                                                                                                                                                                 0; Gaps
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STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FAPILICATION NUMBER: PCT/US92/09487
FILING DATE: 19921104
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 35302
REPRENCE/DOCKET NUMBER: 3113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 946-5750
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 YIEGEMRTRIRYNRRS 198
LENGTH: 267 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-610-838-1
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us-10-083-336a-7.rai

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COUNTRY:
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                                                                                                                                                                                                                                                                                      3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVGL 62
                                                                                                                                                                                                                                               3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                        0; Gaps
                                                                                                                                                            99.1%; Score 1010; DB 5; Length 267; 100.0%; Pred. No. 1.5e-110; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biosynthetic Binding Protein for Cancer
Marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
STREET: Exchange Place, 53 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
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REGISTRATION NUMBER: 27,829
REPERENCE-DOCKET NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 8, Application US/08356786; Patent No. 5877305; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic
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MEDIUM TYPE: FLODBY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 YIEGEMRTRIRYNRRS 198
TYPE: 267 amino acids
TYPE: AMINO ACID
TOPOLOGY: 1:-
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INFORMATION FOR SEQ ID NO: 8:
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                                                                                                                                                        Query Match
Best Local Similarity 100.C
Matches 196; Conservative
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                     SEQUENCE CHARACTERISTICS
                                                                                               MOLECULE TYPE: protein PCT-US92-09487-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-356-786-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
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APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
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                                                                                                                                                                                                                  63 SNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEALTHLFTDVQNRYTFAFGGN 122
                                                                                                                                                                                                                                                     64 SNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 123
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                                                                                                                                                                                                                                                                                                                                              4 PKOYPIINFTTAGATVOSYINFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 63
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                                                                                                                       3 PKOYPIINFITAGAIVOSYTNFIRAVRGRLITGADVRHEIPVLPNRVGLPINORFILVEL
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                                                                         0; Gaps
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                         Length 268;
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Score 1010; DB 2; Lengtn 2000; Pred. No. 1.5e-110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN BOTA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1010; DB 1; I
Pred. No. 1.7e-110;
                         Ouery Match
99.1%; Score 1010; Di
Best Local Similarity 100.0%; Pred. No. 1.5s
Matches 196; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 1.7.
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 27, Application US/08378761A; Patent No. 5635384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
                                                                                                                                                                                                                                                                                                                                                                                                                183 YIEGEMRIRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 YIEGEMRIRIRYNRRS 199
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NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TERENCE A
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MORGAN, ALICE ER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  290 amino acids
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDIANAPOLIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as
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Search completed: February 10, 2004, 16:29:33 Job time: 12.4485 secs

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February 10, 2004, 16:26:46; Search time 25.5389 Seconds (without alignments) 1623.314 Million cell updates/sec
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| cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       801455 seqs, 209382283 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                     protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 7, Appli Sequence 1, Appli	Ä	Sequence 3, Appli	Sequence 10, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 8, Appli	Sequence 4, Appli	Sequence 6, Appli	Sequence 11, Appl	Sequence 9, Appli	Sequence 2, Appli	Sequence 39, Appl
SUMMARIES	US-10-282-935-1	US-10-440-796-1	US-10-083-336A-3	US-10-083-336A-10	US-10-127-890-1	US-10-083-336A-1	US-10-083-336A-8	US-10-083-336A-4	US-10-083-336A-6	US-10-083-336A-11	US-10-083-336A-9	US-10-083-336A-2	US-09-792-793A-39
	12	12	12	12	12	12	12	12	12	12	12	12	10
% Query Match Length DB	198	267	198	200	267	216	188	188	189	190	185	179	247
% Query Match	100.0	100.0	99.1	99.1	99.1	99.1	93.2	92.3	92.3	92.3	7.06	72.4	33.6
Score	1019	1019	1010	1010	1010	1010	950	941	941	941	924.5	738	342
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16 342 33.6 247 12 US-10-127-890-6 19 342 33.6 247 12 US-10-375-209A-39 18 32.42 33.6 247 12 US-10-280-95-3 20 323.5 31.7 251 12 US-10-280-95-3 21 31.7 251 12 US-10-280-95-3 22 31.7 251 12 US-10-280-95-3 23 30.6 247 10 US-09-792-793A-34 23 27.2 263 12 US-10-7480-796-3 24 27.7 27.2 263 12 US-10-127-890-7 25 27.2 263 12 US-10-127-890-7 26 27.7 27.2 24.1 25.1 12 US-10-127-890-10 26 27.7 27.2 25.1 12 US-10-127-890-10 27 27.2 25.1 12 US-10-127-890-10 28 24.1 25.1 12 U	Sequence 6, Appli Sequence 39, Appl Sequence 4, Appli Sequence 3, Appli Sequence 34, Appli Sequence 34, Appli Sequence 34, Appli	47 28 24	14611140	Sequence 102, App Sequence 103, App Sequence 105, App Sequence 1, Appli Sequence 1, Appli Sequence 109, App Sequence 259, App Sequence 259, App
323.36 3422 3422 323.422 323.422 323.422 323.422 333.6 333.7	12 US-10-127-890- 12 US-10-375-209A 12 US-10-280-679B 12 US-10-282-935- 12 US-10-440-796- 10 US-99-792-793A 12 US-10-375-209A	1220045		44444466
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ALIGNMENTS

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                                                                                                                    APPLICANT: Olson, Mark A
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REPERBNCE: P67452US0 (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
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                                    Sequence 7, Application US/10083336A Publication No. US20030181665A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Ricinus communis US-10-083-336A-7
RESULT 1
US-10-083-336A-7
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TYPE: PRT
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APPLICANT: GHETIE, VICTOR F.
APPLICANT: SMALLSHAW, JOAN
APPLICANT: SMALLSHAW, JOAN
APPLICANT: SMALLSHAW, JOAN
APPLICANT: BALUNA, ROXANA
APPLICANT: BALUNA, ROXANA
APPLICANT: BALUNA, ROXANA
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
TITLE OF INVENTION: PROTEINACEOUS COMFOUNDS
CURRENT APPLICATION NUMBER: US/10/292,935
PRIOR APPLICATION NUMBER: 09/538,873
PRIOR APPLICATION NUMBER: 60/126,826
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
SUTMERR OF SEQ ID NOS: 23
SOFTWARE: PATENTIN VEY: 2.1
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APPLICANT: GHETIE, VICTOR F.
APPLICANT: SMALLSHAW, JOAN
APPLICANT: SMALLSHAW, JOAN
APPLICANT: BALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
TITLE OF INVENTION: SYNDROME (VLS)
FILE REFERENCE: UTSD: 603
CURRENT APPLICATION NUMBER: US/10/440,796
CURRENT APPLICATION NUMBER: US/10/440,796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US/09/538,873
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/126,826
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 19
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                                                                                                                                           Sequence 1, Application US/10282935
Publication No. US20030143193A1
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                            FOYIEGEMRTRIRYNRRS 198
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APPLICANT: VITETTA, ELLEN S. APPLICANT: GHETIE, VICTOR F.
                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Olson, Mark A
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher: Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452USO (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT APPLICATION NUMBER: US/10/083,336A
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                  1 MVPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
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                                                                                                                                                                                                                                                                                            Length 267;
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                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                                                            100.0%; Score 1019; DB 12; 100.0%; Pred. No. 2.2e-108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 99.1%; Score 1010; DB 12; Best Local Similarity 100.0%; Pred. No. 1.5e-107; Matches 196; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/10083336A, Publication No. US20030181665A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 FQYIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 FOYIEGEMETRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 YIEGEMRTRIRYNRRS 198
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                                                 LENGTH: 267
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                       Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Ricinus communis
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
US-10-083-336A-3
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LENGTH: 198
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123 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182
64 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PHILING DATE: 09-DEC-1992
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/646,360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 12-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 267 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                   183 YIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                184 YIEGEMRIRIRYNRRS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 650 388-1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                 US-10-127-890-1
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                                                                                                             APPLICANT: Olson, Mark A
APPLICANT: Milard, Charles B
APPLICANT: Milard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452USO (RILD 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.1
ENGTHA: 199
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APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452USO (RID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.1%; Score 1010; DB 12; Length 199; 100.0%; Pred. No. 1.5e-107; ive 0; Mismatches 0; Indels 0
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                                  Sequence 5, Application US/10083336A Publication No. US20030181665A1 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Ricinus communis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Ricinus communis
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Best Local Similarity 100.
Matches 196; Conservative
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                  US-10-083-336A-5
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LENGTH: 200
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Best Local S
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124 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFØ 183
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                                                                                                                                                                                                                                     Sequence 1, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSE: NCAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 99.1%; Score 1010; DB 12; Best Local Similarity 100.0%; Pred. No. 2.4e-107; Matches 196; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
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                                                                                                             63 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
                                                                                                                                                                                     123 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182
                                                                                                                                                                                                                      38 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 97
                              62
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APPLICANT: Olson, Max.
APPLICANT: Millard, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Wanneacher. Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REPERENCE: P67452US0 (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2022-05-21
NUMBER OF SEQ ID NOS: 15
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APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Byrne, Michael P
APPLICANT: Byrne, Michael P
APPLICANT: Byrne, Michael P
APPLICANT: Bobert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452US0 (RIID 01-58)
FURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
63 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
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99.1%; Score 1010; DB 12; Length 576;
Best Local Similarity 100.0%; Pred. No. 7.1e-107;
Matches 196; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/10083336A; Publication No. US20030181665A1
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SEQ ID NO 1
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63 SNHABELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
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APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Mannemacher. Robert W
APPLICANT: Wannemacher. Robert W
APPLICANT: Wannemacher. Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452USO (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 202-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
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Pred. No. 1.2e-99;
0; Mismatches 0; Indels 1
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94.9%; Pred. No. 1.1e-100;
tive 0; Mismatches 0;
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Best Local Similarity 94.9%;
Matches 186; Conservative 0
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ORGANISM: Ricinus communis
                                                               ORGANISM: Ricinus communis
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Matches 188; Conservative
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US-10-083-336A-6
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US-10-083-336A-4
                 LENGTH: 188
TYPE: PRT
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                                                                                                                                           Query Match
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SEQ ID NO 8
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114 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 173
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Best Local Similarity 93.43
Matches 183; Conservative
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                APPLICANT: Olson, Mark A
APPLICANT: Milard, Charles B
APPLICANT: Milard, Charles B
APPLICANT: Michael P
APPLICANT: Wannemacher, Robert W
APPLICANTON: NUMBER: US/10/083,336A
CURRENT APPLICATION NUMBER: US/10/083,336A
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
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APPLICANT: Byrne, Michael P
APPLICANT: Byrne, Michael P
APPLICANT: Byrne, Michael P
APPLICANT: Byrne, Michael P
TILLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452US0 (RILD 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
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US-10-083-336A-6
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ORGANISM: Ricinus communis
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Best Local Similarity
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GENERAL INFORMATION:
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US-10-083-336A-11
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LENGTH: 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Olson, Mark A
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452USO (RIID 01-58)
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Byrne, Michael P
APPLICANT: Byrne, Michael P
TILLE OF INVENTION: Richard and Methods of Making and Using Thereof
FILE REFERENCE: P67452USO (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
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                                                                                                                                                                                                      Sequence 9, Application US/10083336A Publication No. US20030181665A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/10083336A Publication No. US20030181665A1 GENERAL INFORMATION:
183 YIEGEMRTRIRYNRRS 198
                                                         174 YIEGEMRTRIRYNRRS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 YIEGEMRIRIRYNRRS 198
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RESULT 15
US-09-792-793A-39
US-09-792-793A-39

US-09-792-793-39

Sequence 39, Application US/09792793A

Patent No. US20020168370A1

GENERAL INFORMATION:

APPLICANT: McDonald, John R.

APPLICANT: Coggins, Philip

TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS

FILE REFERENCE: 25020-601D

CURRENT APPLICATION NUMBER: US/09/792,793A

CURRENT FILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 93

SOFTWARE: PATENTIN VEY: 2.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 TISVAIDVTNVYIMGYRAGDISYFF---NEASATEAAKYVFKDAMRKVTLPYSGNYERLQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 SVTLALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VSFRLSGATSSSYGVFISNLRKALPNERKL-YDIPLL--RSSLPGSQRYALIHLTNYADE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 INFITAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 68
3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 62
                         38 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 33.6%; Score 342; DB 10; Length 247; Best Local Similarity 39.5%; Pred. No. 9.4e-31; Matches 73; Conservative 46; Mismatches 54; Indels 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: February 10, 2004, 16:53:53 Job time : 25.5389 secs
                                                                                                                                                                           123 YDRLEQLAGNLRENIELGNGPL 144
                                                                                                                                                                                                                158 YDRLEQLAGNIRENIELGNGPL 179
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LENGTH: 247
TYPE: PRT
ORGANISM: Trichosanthews kirilowii
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

February 10, 2004, 16:17:35; Search time 10.7146 Seconds (without alignments) 1777.145 Million cell updates/sec

US-10-083-336A-7

1019 1 MVFKQYPIINFTTAGATVQS.....ARFQYIEGEMRTRIRYNRRS 198 Perfect score: Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

283308 Total number of hits satisfying chosen parameters:

283308 seqs, 96168682 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Listing first 45 summaries Maximum Match 100% Post-processing: Minimum Match 0%

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		٠			SOMMAKIES	
Result No.	Score	Query Match	Length	DB	ID	Description
 	1010	99.1	576	1	RLCSD	ricin D precursor
7	N	90.3	564		RLCSAG	17
٣	353.5	34.7	528		S32431	abrin-d precursor
4	5	34.7	562		S16022	
Ŋ	345		527		S32430	abrin-b precursor
9	342		289		RLTZT	rRNA N-glycosidase
7	338	33.2	247		JU0393	karasurin - Mongol
80	338		247		JC5032	karasurin-B - Tric
6	338		289		JC5606	karasurin C - Tric
10	3		251		C39761	abrin (clone 7.2)
11	N		528		TZLSA	abrin-a precursor
12	307.5		278		\$23519	beta-luffin - smoo
13	0	29.5	250		JN0108	luffin-b - smooth
14	291		570		S62627	agglutinin I precu
15	286		254		PD0018	mistletoe lectin I
16	284.5		277		S22494	rRNA N-glycosidase
17	281	27.6	286	7	S25560	rRNA N-glycosidase
18	278	27.3			JC4840	rRNA N-glycosidase
19	277	27.2			RLPUGG	
20	274	7			JC4235	rRNA N-glycosidase
21	242.5	23			JT0753	rRNA N-glycosidase
22	197.5	19.4	294		S28421	rRNA N-glycosidase
23	182	17.9	313		S17757	rRNA N-glycosidase
24	180.5	17.7	261		JE0401	antiviral protein
25.	178	17.5	278		A39817	(3
26	156	•	272		JC4811	betavulgin - beet
27	149.5	14.7	289		T12573	rRNA N-glycosidase
28	140	13.7	280		RLBH	rRNA N-glycosidase
29	137	13.4	275	7	833631	tritin - wheat

30K ribosome inact	protein synthesis	rRNA N-glycosidase	ribosome-inactivat	rRNA N-glycosidase	rRNA N-glycosidase	shiga-like toxin I	Shiga toxin 2 subu	Shiga toxin 2 subu	Shiga-like toxin I	rRNA N-glycosidase					
B38664	JC5848	528542	528539	S29931	805205	S17519	S28541	846239	RLQHG2	A58923	I54695	E90779	G85640	801032	S17932
7	ď	N	N	7	N	N	N	N	Н	N	7	7	N	~	7
281	280	253	253	253	283	293	253	310	292	253	319	319	319	318	236
13.1	13.0	12.9	12.5	12.5	12.2	12.1	12.1	12.1	11.9	11.3	10.9	10.9	10.9	10.8	10.8
133	132	131	127	127	124	123.5	123	123	121	115	111	111	111	110.5	110
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RLCSD
	ricin D precursor - castor bean
	N;Contains: rRNA N-glycosidase (EC 3.2.2.2)
	C;Species: Ricinus communis (castor bean)
	C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 16-Jul-1999
_	C;Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903
	R; Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver,
	Nucleic Acids Res. 13, 8019-8033, 1985
	A, Title: Genomic cloning and characterization of a ricin gene from Ricinus communi
	A; Reference number: A24041; MUID:86067214; PMID:2999712
	A;Accession: A24041
	A; Molecule type: DNA
	A; Residues: 1-576 < HAL>
	A; Cross-references: GB: X03179; NID: 921082; PIDN: CAA26939.1; PID: 921083
	R;Tregear, J.W.; Roberts, L.M.
	Plant Mol. Biol. 18, 515-525, 1992
	A, Title: The lectin gene family of Ricinus communis: cloning of a functional ricir

R. F. 18.

A; Reference number: \$20513; MUID: 92163016; PMID: 1371405

A;Accession: S20513

A,Molecule type: DNA
A,Residues: 1-576 <TRE>
A,Cross-references: EMBL:X52908; NID:g21084; PIDN:CAA37095.1; PID:g21085
B,Lamb, F.I.; Roberts, L.M.; Lord, J.M.
Bur. J. Biochem. 148, 265-270, 1985
A,Title: Nucleotide sequence of cloned cDNA coding for preproricin.
A,Reference number: A24614; MUID:85179479; PMID:3838723

A; Accession: A24614

A Molecule type: mRNA A Residues: 12-75, 10', 77-550, R',552-576 <LAM> A; Residues: 12-75, 10', 77-550, R', 1552-576 <LAM> A; Cross-references: GB:XO2388; NID:g21077; PIDN:CAA26230.1; PID:g21078 R; Yoshitake, S.; Funatsu, G.; Funatsu, M. R; Yoshitake, S.; Funatsu, G.; Funatsu, M. A; Yitle: Isolation and sequences of peptic peptides, and the complete sequence of Ile characterince number: A03372

A, Accession: A03372

A; Accession: A24010

A,Molecule type: protein A,Residues: 315-383,'PS',386-576 <ARA> R,Funatsu, G.; Kimura, M.; Funatsu, M. Agric. Biol. Chem. 43, 221-2224, 1979 A,Title: Primary structure of Ala chain of ricin D. A,Reference number: A03374

A; Molecule type: protein

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A; Contents: autocartus, active stree
A; Futtenber, E; Robertus, J.D.
Proteins 10, 260-269, 1991
A; Title: Structure of ricin B-chain at 2.5 angstroms
A; Reference number: A48238; MUID:3132005; PMID:1881882
A; Contents: annotation; X-ray crystallography, 2.5 angstroms
A; Reference number: A48239; MUID:91352004; PMID:1881881
A; Title: Structure of ricin A-chain at 2.5 angstroms
A; Reference number: A48239; MUID:91352004; PMID:1881881
A; Contents: annotation; X-ray crystallography, 2.5 angstroms
A; Reference number: A48239; MUID:91352004; PMID:1881881
A; Conment: The functional molecule is a disultide-linked dimer of A and B chains, A; Comment: The A chain; B chains are also responsible for cell agglutination (1-c; Comment: The A chain; B chains are also responsible for cell agglutination (1-c; Comment: This protein is cytocoxic and very poisonous to animals.
C; Comment: This protein is cytocoxic and very poisonous to animals.
C; Comment: This protein is cytocoxic and very poisonous to animals.
C; Superfamily: ricin; PRNA N-91ycosidase homology
C; Keywords: duplication; glycoprotein; glycosidase, hydrolase; lectin; RNA binding; seed
F; 13-57 Domain: signal sequence #status predicted <SIG>F; 6-293 Domain: RNA N-91ycosidase homology <RNG>F; 6-293 Domain: RNA N-91ycosidase homology <RNG
F; 6-4949 Penduct: ricin D chain B #status experimental <BCH>F; 6-4949 Pending site: carbohydrate (fyr, Tyr, Glu, Asn) #status seperimental
F; 11-15-2449 Pending site: carbohydrate (fyr, Tyr, Glu, Asn) #status seperimental
Proteins 10, 270-278, 1991
A;Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism A;Title: Site-directed mutagenesis of Ficin A-chain and implications for the mechanism A;Reference number: A48237; MUID:91352006; PMID:1881883
A;Contents: annotation; active site
R;Rutenber, E.; Robertus, J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nicontains: FRNA Niglycosidase (EC 3.2.2.2)
Species: Ricinus communis (castor bean)
Cispecies: Alcinus communis acquire (cispecies: Luni Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.
Richetts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.
A.Reference number: A24261, MUID:86059449; PMID:2998130
A.Rocession: A24261
A.Rocession: 
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100.0%; Pre
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Matches 196; Conserv
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CjAccession: S32431; S34408
R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
Wol. Biol. 229, 263-267, 1993
A;Title: Primary structure of three distinct isoabrins determined by cDNA sequencing. Co
A;Reference number: S32429; MUID:93132798; PMID:8421313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivatin The A and B chains are linked by a single disulfide bond, which is essential for toxicit C;Superfamily: ricin; TRNA N-glycosidase homology C;Superfamily: ricin; TRNA N-glycosidase homology C;Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; p F;1-251/Product: abrin-d chain A #status predicted <ACH>
                                                                                                                                                                                                                                   A;Molecule type: protein
A;Molecule type: protein has strong agglutinating activity and weak cytotoxicity compared
C;Comment: This protein has strong agglutinating activity and weak cytotoxicity compared
C;Guperfamily: rich; rRNA N-glycosidase homology
C;Keywords: duplication; glycoprotein; glycosidase, hydrolase; lectin; RNA binding; seed
F;1-24/Domain: signal sequence #status predicted <ACH>
F;35-29/Product: agglutinin chain A #status predicted <ACH>
F;35-29/Product: agglutinin chain B #status experiental <BCH>
F;30-364/Product: agglutinin chain B #status experiental <BCH>
F;30-364/Product: agglutinin chain B #status predicted
F;30-364/Product: agglutinin chain B #status predicted
F;30-364/Product: agruting site: substrate (Apr) (covalent) #status predicted
F;30-363/Active site: Glu, Arg #status predicted
F;30,23/Active site: Glu, Arg #status predicted
F;20,23/Active site: Glu, Arg #status predicted
F;30,35/Active site: Carbohydrate (Asp) (covalent) #status experimental
F;336,557/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
Araki, T.; Yoshioka, Y.; Punatsu, G.
iochim. Biophys. Acta 872, 277-285, 1986
Title: The complete amino acid sequence of the B-chain of the Ricinus communis aggluti.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 SNHABLSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 SNHAELSVILALDVINAYVVGCRAGNSAYFFHPDNQEDAEAITHLFIDVQNSFIFAFGGN 146
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C;Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 PKQYPIINPTTADATVESYTNFIRAVRSHLTTGADVRHEIPVLPNRVGLPISQRFILVEL
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60
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N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        206 YIEGEMRTRIRYNRRS 221
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                                                                                                                                                A; Reference number: A24210
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A; Residues: 1-528 <HUN>
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          R;Araki,
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A;Molecule type: protein
A;Residues: 260-281, D', 283-290, N', 292-349, 'PQ', 352-377, 'N', 379-425, 'M', 427, 'D', 429-430,
A;Experimental source: seed
C;Superfamily: ricin; rRNA N-glycosidase homology
C;Reywords: disulfade bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; p)
F;1-250/Product: abrin-b chain A #status predicted <ACH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Title: Primary structure of three distinct isoabrins determined by cDNA sequencing. Cor A,Reference number: S32429; MUID:93132798; PMID:8421313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Kimura, M.; Sumizawa, T.; Funatsu, G.
Biosci. Biothem. 57, 166-169, 1993
A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, A;Reference number: JC1398; MUID:93169023; PMID:7763422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 HAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 124
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                                                   125 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 184
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F;7-245/Domain: rRNA N-glycosidase homology <RNG>
F;260-527/Product: abrin-b chain B #status experimental <BCH>
F;282-324,325-365,368-406,413-448,452-491,494-527/Region: 40-residue repeats
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;74,113,194,195/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predict
F;110,360,400/Binding site: carboxydrate (Asn) (covalent) #status predicted
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F;246-268,285-304,328-345,416-429,455-472/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 20-Aug-1999 C;Date: 30-480; JC1399 C;Accession: $23430; JC1399 T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
                                                                                              1 ODGVIKFTTEGATSOSYKOFIEALRORLIGG--LIHGIPVLPDPTTLOERNRYISVELSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB: M98345; NID:g166296; PIDN: AAA32625.1; PID:g166297
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2.9e-23;
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Pred. No. 2
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45.5%;
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Best Local Similarity
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A; Residues: 1-527 <HUN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Accession: S16022
R;Wood, K.A.; Lord, J.M.; Wawrzynczak, E.J.; Piatak, M.
R;Wood, K.A.; Lord, J.M.; Wawrzynczak, E.J.; Piatak, M.
R;Ur. J. Biochem. 198, 723-732, 1991
A;Title: Preproabrin: genomic cloning, characterisation and the expression of the A-chai A;Reference number: S16022; MUID:91266957; PMID:2050149
A;Accession: S16022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cikeywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglutamic acid fish-286/Product: abrin-c chain A #status predicted <ACH->P.55-286/Product: abrin-c chain B #status predicted <ACH->P.51-280/Domain: rRNA N-glycoladase homology cacid <ACH->P.51-280/Domain: rRNA N-glycoladase homology redicted <ACH->P.51-280/Domain: rRNA N-glycoladase homology cacid <ACH->P.51-280/Product: abrin-c chain B #status predicted <ACH->P.51-280, 280-480, 403-441, 448-483, 487-526, 529-562/Region: 40-residue repeats P:31-359, 360-480, 403-441, 448-483, 487-526, 529-562/Region: 40-residue repeats P:108 147, 229, 230/Bainding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted P:108 147, 229, 230/Bainding site: substrate (Arn) (covalent) #status predicted P:281-303, 320-339, 363-380, 451-464, 480-507/Disulfide bonds: #status predicted P:322, 346/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating The A and B chains are linked by a single disulfide bond, which is essential for toxicial. Superfamily: ricin; rRNA N-glycosidase homology
F;283-325,326-366,369-407,414-449,453-492,495-528/Region: 40-residue repeats F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted F;1/Modified site: substrate (Tyr, Tyr, Glu, Asn) #status predicted F;164,113,195,196/Binding site: substrate predicted F;200,253,361,401,402/Binding site: carbohydrate (Asn) (covalent) #status predicted F;200,253,361,401,402/Binding site: carbohydrate (Asn) (covalent) #status predicted F;288,312/Binding site: N-acety1galactosamine (Asp, Asn) #status predicted F;500,521/Binding site: N-acety1galactosamine (Asp, Asn) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 HAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 SERESIEVGIDVINAYVVAYRAGSQSYFL---RDAPASASTYLFPGTQ-RYSLRFDGSYG 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 HAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYIFAFGGNYD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 QYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ODQVIKFTTEGATSQSYKQFIEALKQKLTGG--LIHDIPVLPDPTTVEERNRYITVELSN 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          abrin-c precursor - Indian licorice
N;Contains: RRNA Nglycosidase (EC 3.2.2.22)
C;Species: Abrus precatorius (Indian licorice)
C;Species: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;534,555/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
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A;Cross-references: EMBL:X55667; NID:g16084; PIDN:CAA39202.1; PID:g16085
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                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 528;
                                                                                                                                                                                                                                                                                                                                               34.7%; Score 353.5; DB 2; Length 945.5%; Pred. No. 5e-24;
ive 24; Mismatches 70; Indels
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Best Local S
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CiSpecies: Trichosanthes kirilowii var. japonica
CiDate: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 23-May-1997
CiAccession: dC5032
Rikondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.
Biol. Pharm. Bull. 19, 1485-1488, 1396
A:Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and ka
A;Reference number: JC5032; MUID:97108848; PMID:8951169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Karasurin - Mongolian snake-gourd
C;Species: Trichosanthes kirilowii (Mongolian snake-gourd)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 12-Apr-1995
C;Accession: JU0393; PS0163
R;Toyokawa, S.; Takeda, T.; Kato, Y.; Wakabayashi, K.; Ogihara, Y.
Chem. Pharm. Bull. 39, 1244-1249, 1991
A;Title: The complete amino acid sequence of an abortifacient protein, karasurin. A;Reference number: JU0393; MUID:92005921; PMID:1914000
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                                                                                                                                                                                                                                                                                                         69 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 127
                                                                                                                                                                                                                                                                                                                                                                                               138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 SVTLALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFIDVQNRYIFAFGGNYDRLE 127
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                                                                                                                                       9 INFITAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 68
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                                                                                                                                                                                             82 IISVAIDVINVYIMGYRAGDISYFF---NEASATEAAKYVFKDAMRKVTLPYSGNYERLQ
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                                                               12; Gaps
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A;Residues: 1-247 <TOY>
A;Note: a sequence which lacks Ala-247 is also shown in this publication
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C;Keywords: abortifacient
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Pred. No. 2.5e-23;
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                                                               46;
                      39.5%;
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Matches 74; Conservative
                                                               Conservative
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A,Molecule type: protein
A,Residues: 1-247 <KON>
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             Best Local Similarity
Matches 73; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 IGKRV 198
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A,Experimental source: tuber 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Molecule type: DNA
A.Residues: 1-72, VV, 74-90, S, 92-233, TV, 235-267, DV, 269-289 <ZHE>
A.Cross-references: GB:S70176; NID:g547148; PIDN:AAB31048.1; PID:g547149
R.Collins, E.J.; Robertus, J.D.; LoPresti, M.; Stone, K.L.; Williams, K.R.; Wu, P.; Hwan
A.D. Blol. Chem. 265, 8665, 1990
A.Title: Primary amino acid sequence of alpha-trichosanthin and molecular models for abr
A.Reference number: A36273; MUID:90256789; PMID:2341399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: protein
A,Residues: 24-270 <CCD>
Kwang, Y. Qian, R.Q.; Gu, Z.W.; Jin, S.W.; Zhang, L.Q.; Xia, Z.X.; Tian, G.Y.; Ni, C.Z
Pre Appl. Chem. 58, 789-798, 1986
A,Title: Scientific evaluation of Tian Hua Fen (THF): history, chemistry and application
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A; Molecule type: protein
A; Mesidues: 24-56, 14, 58-59, 17, 61-71, 17, 73-81, 85-86, 17, 88-92, DAGLPRNAVL, 93-142, GL'
A; Experimental source: tuber
R; Huang, Q: Liu, S:; Tang, Y:; Jin, S:; Wang, Y:
Bubmitted to the Brookhaven Protein Data Bank, July 1994
A; Reference number: A67091; PDB:1MRJ
A; Contents: annotation; X-ray crystallography, 1.6 angstroms, with adenine, residues 24-87; Huang, Q: Liu, S:; Tang, Y:, Jin, S:; Wang, Y:
Submitted to the Brookhaven Protein Data Bank, July 1994
A; Reference number: A67092; PDB:1MRK
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             C;Date: 30-Sep-1988 #sequence_revision 26-Jan-1996 #text_change 23-Mar-2001 C;Accession: 470566; A36274; JC1093; A36273; JT0003 R;Shaw, P.C.; Yung, M.H.; Zhu, R.H.; Ho, W.K.K.; Ng, T.B.; Yeung, H.W. Gene 97, 267-272, 1991
A;Title: 10noing of trichosanthin cDNA and its expression in Escherichia coli. A;Reference number: JT0566; MUID:91153657; PMID:1999291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology C; Superfamily: rRNA N-glycosidase; hydrolase; root; toxin C; Keywords: abortifacient; glycosidase; hydrolase; root; toxin F; 1-23/Domain: signal sequence #status predicted <SIG> F; 24-270/Product: trichosanthin alpha #status experimental <MAT> F; 72-66/Domain: rRNA N-glycosidase homology <RNG> F; 71-289/Domain: rarboxyl-terminal propeptide #status predicted <CTP> F; 93,183,186/Active site: Tyr, Glu, Arg #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Reference number: A58622; MUID:95360114; PMID:7634073
A.Contents: annotation; X-ray crystallography, 1.7 angstroms
C.Comment: Alpha-trichosanthin has been used to induce abortions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.Xiong, J.P.; Xia, Z.X.; Wang, Y. submitted to the Brookhaven Protein Data Bank, December 1994 A.Reference number: A66711; PDB:1TCS
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A;Accession: JT0003
                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-289 <SHA>
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33.6%; Score 342; DB 1; Length 289;

Query Match

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N; Contains: rRNA Nglycosidase (EC 3.2.22)
C; Species: Abrus precatorius (Indian licorice)
C; Species: Abrus precatorius (Indian licorice)
C; Date: 31-Dec-1993 #sequence revision 01-Aug-1997 #text change 16-Jul-1999
C; Accession: S32429; JT0202; A39761; JC1398; S14472; S24T33; S74110; S74111
R; Hug, C; H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
A; Title: Primary structure of three distinct isoabrins determined by CDNA sequencing. Cor
                                                                                                                                                      abrin (clone 7.2) precursor - Indian licorice (fragment)
N;Contains: rRNA N-glycosidase (EC 3.2.2.2)
S;Species: Abrus preadrorius (Indian licorice)
C;Species: Abrus preadrorius (Indian licorice)
C;Accession: C39761; 814471
R;Evensen, G.; Mathiesen, A.; Sundan, A.
Biol. Chem. 266, 6848-6852, 1991
A;Fitle: Direct molecular cloning and expression of two distinct abrin A-chains.
A;Reference number: A39761; MUID:91201329; PMID:2016300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Molecule type: DNA

A; Residues: 'M',1-251 < EV2>

A; Cross-references: EMBL:X54872; NID:g16088; PIDN:CAA38654.1; PID:g16089

A; Cross-references: EMBL:X54872; NID:g16088; PIDN:CAA38654.1; PID:g16089

C; Superfamily: ricin; rRNA N-glycosidase homology

C; Keywords: duplication; glycosidase; hydrolase; lectin; toxin

F; 1-251/Product: abrin (Glone 7.2) chain A #status predicted <ACH>

F; 7-246/Domain: rRNA N-glycosidase homology < RNG>

F; 7-246/Domain: rRNA N-glycosidase homology < RNG>

F; 7-13,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted

F; 164,167/Active site: Glu, Arg #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 LAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 188
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A; Residues: 'E',2-528 cHUN>
A; Residues: 'E',2-528 cHUN>
A; Cross-references: GB: M98344; NID: 9166294; PIDN: AAA32624.1; PID: 9166295
A; Cross-references: GB: M98344; NID: 9166294; PIDN: AAA32624.1; PID: 9166295
A; Cross-references: GB: M98344; NID: 9166294; PIDN: AAA32624.1; PID: 9166295
A; Note: residues 1-8 were derived from the synthesized primer
A; Funatsu, G.; Taguchi, Y.; Kamenosono, M.; Yanaka, M.
Agric. Biol. Chem. 52, 1095-1097, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1.51. EVE>
R;Evensen, G.; Mathiesen, A.; Sundan, A.
submitted to the EMBL Data Library, October 1990
A;Description: Direct molecular cloning of two distinct abrin A-chains.
A;Reference number: S14471
A;Accession: S14471
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A;Accession: S32429
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   194 IGKRV 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: DDBJ:AB000666; NID:g2329830; PIDN:BAA21786.1; PID:g2329831
R;Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.
Biol. Pharm. Bull. 19; 1485-1489; 1996
A;Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and ka A;Reference number: UC5032; MUID:97108848; PMID:8951169
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F; 24-270/Product: karasurin A #etatus predicted <AMA>
C;Comment: This protein belongs to type I ribosomal-inactivating proteins which catalyti
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;4-243/Domain: rRNA N-glycosidase homology <RNG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 IISVAIDVINVYVMGYRAGDTSYFF---NEASATEAAKYVFKDAKRKVTLPYSGNYERLQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 IAAGKIRENIPLGLPALDSAITTLFYYNAN-----SAASALMVLIQSTSEAARYKFIBQQ 170
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                                                                                                                                                                                                                                                                                                                                                 28
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                                                                                                                                    33.2%; Score 338; DB 2; Length 247; 40.0%; Pred. No. 4.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53; Indels
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                                                                                                                                                                                                            74; Conservative
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A;Molecule type: protein
A;Residues: 22-270 <KON>
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                                                                                                                                           Query Match
Best Local Similarity
Matches 74; Conserv
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A; Residues: 1-289 <MIZ>
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IGKRV 175
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luffin-b - smooth loofah
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 262-276, X, 7, 278-280; 329-348; 369-388; 399-418 < LIW>
A; Residues: 262-276, X, 7, 278-280; 329-348; 369-388; 399-418 < LIW>
A; Experimental source: seed
C; Comment: Abrin-a is more toxic than ricin. The toxin consists of an A chain, which inh taining receptors on the cell surface. The A and B chains are linked by a single disulfic, Superfamily: ricin; rNAA N-91ycosidase homology
C; Superfamily: ricin; rNAA N-91ycosidase homology
F; 251/Product: abrin-a chain A #status experimental <ACH>
F; 246/Domain: rNAA N-91ycosidase homology <RNG>
F; 2851/Product: abrin-a chain B #status experimental <BCH>
F; 283-225, 326-366, 369-407, 414-449, 453-492, 4955-528/Region: 40-residue repeats
F; 1/Modified site: pyrrolidone carboxylic acid (GIn) #status experimental
F; 74, 113, 195, 196 Binding site: substrate (Tyr, Tyr, GIu, Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 'E',2-21 cEVE>
A; Cross-references: GB:X54872
A; Cross-references: GB:X54873
A; Cross-references: GB:X54873
A; Cross-residues: 1-8 were derived from the synthesized primer
B; Kimura, M.; Sumizawa, T.; Funateu, G.
Biosci: Biotechnol. Biochem. 57, 166-169, 1993
A; Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic
A; Reference number: JC1398; MUID:93169023; PMID:7763422
A; Contents: seeds
                                                                                                                                                                                                                  A,Molecule type: protein
A,Rolecule type: protein
A,Rolecule type: 1-201,203-251 <FUN>
A,Rolecule type: T-201,203-251 <FUN>
A,Rolecule the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have R,Evensen, G.; Mathiesen, A.; Sundan, A.
J. Biol. Chem. 266, 6848-6852, 1991
A,Title: Direct molecular cloning and expression of two distinct abrin A-chains.
A,Reference number: A39761; MUID:91201329; PMID:2016300
A,Accession: A39761
A,Status; nucleic acid sequence not shown
A,Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein A,Reference number: JT0202
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F,247-269,286-305,329-346,417-430,456-473/Disulfide bonds: #status predicted
F,288,312/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
F,361,401/Binding site: carbohydrate (Asn) (covalent) #status experimental
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A.Molecule type: protein
A.Rocession: JC1397
A.Rocession: JC1398
A.Molecule type: protein
A.Rocession: 261-347,'r',349-351,'A',353-357,'L',359-528 «KIM»
A.Rocession: 261-347,'r',349-351,'A',353-357,'L',359-528 «KIM»
A.Rocession: C. Mathiesen, A.; Sundan, A.
Submitted to the EMBL Data Library, October 1990
A.Reference number: S14471
A.Reference number: S14471
A.Reference number: S14472
A.Rocession: ME', 2-251 «FWV2»
A.Rocession: S14472
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A; Residues: 262-297, Y', 299-426, 'L', 428-466, 'P', 468-482, 'L', 484-528 < CH

R; Lin, S.H.; Chow, L.P.; Chen, Y.L.; Liaw, Y.C.; Chen, J.K.; Lin, J.Y.

Bur. J. Biochem. 240, 564-569, 1996

A; Title: Probing the domain structure of abrin-a by tryptic digestion.

A; Reference number: S74110; MUID: 97008945; PMID: 8856055
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A, Residues: 89-108;154-172 <
A, Experimental source: seed
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Gaps

Indels 13;

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C;Accession: $23519; $23113 -
R;Kataoka, U.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.
Plant Mol. Biol. 19, 887-7889, 1992
A;Title: Nucleotide sequence of cDNA encoding beta-luffin, another ribosome-inactivating
A;Reference number: $23519; MUID:92353400; PMID:1643290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 128
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                                                                                                                                   SVILALDVINAYVVGYRAGNSAYFFH--PDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL 126
                                                                                                                                                                                                                                                                           127 EQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG 186
                                                                                                                                                                                                                                                                                                                   68
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68
                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deta-luffin - smooth loofah
C;Species: Luffa cylindrica (smooth loofah)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Aug-1999
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C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 07-May-1999
                                5 IXFSTEGATSQSYKQFIEALRERLRGG--LIHDIPVLPDPTTLQERNRYITVELSNSDTE
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                                                                                                                                                                                                         63 SIEVGIDVINAYVAYRAĞIQSYFLRDAPSSASD----YLFIGI-DQHSLPFYGIYGDL
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A;Cross-treferences: EMBL;X62372; NID:g19149; PIDN:CAA44230.1; PID:g19150
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;26-264/Domain: rRNA N-glycosidase homology «RNG»
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A,Molecule type: protein
A,Residues: 1-250 <1SL>
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;5-246/Domain: rRNA N-glycosidase homology
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R;Islam, M.R.; Hirayama, H.; Funatsu, G.
Agric. Biol. Chem. 55, 229-238, 1991
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A;Title: Primary structure and molecular modeling of mistletoe lectin I from Viscum albu A;Reference number: PD0018; MUID:98308123; PMID:9642133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agglutinin I precursor - European elder
C.Species: Sambucus nigra (European elder)
C.Species: Sambucus nigra (European elder)
C.Species: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999
C.Accession: 862627; 865619
R.van Damme, E.J.M.; Barre, A.; Rouge, P.; van Leuven, F.; Peumans, W.J.
Blochem. 235, 128-137, 1996
A;Title: The NeuAc(alpha-2,6)-Gal/GalNAc-binding lectin from elderberry (Sambucus nigra)
A;Reference number: 862619; MUID:96202926; PMID:8631319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                       129 LAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIOMISEAARFQYIEGEM 188
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                                                                                                                                                                             69 SVTLALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 128
                                                                                      3 VSFSLSGADSKSYSKFITALRKALPSKEKVSNIPLLLPSASGA---SRYILMQLSNYDAK 59
                                                          9 INFITAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: EMBL:U27122; NID:g1141772; PIDN:AAC49158.1; PID:g1141773
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C;Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 26-Aug-1999
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                     Gaps
                     11;
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                     64; Indels
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; Pred. No. 1.1e-19; 48; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Molecule type: protein
A.Residues: 29-39;39;309-313 <VA2>
C.Superfamily: ricin; rRNA N-91ycosidase homology
F;37-283/Domain: rRNA N-91ycosidase homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 39.0%; Pred. No. 2.4e-
nes 76; Conservative 33; Mismatches
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  34.28;
                       64; Conservative
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  Best Local Similarity
Matches 64; Conserva
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A;Molecule type: mRNA
A;Residues: 1-570 <VAN>
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

February 10, 2004, 16:13:55; Search time 6.60489 Seconds (without alignments) 1409.756 Million cell updates/sec

US-10-083-336A-7 1019 1 MVPKQYPIINFTTAGATVOS.....ARFQYIEGEMRTRIRYNRRS 198 Title: Perfect score: 1 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	CI		AGGL_RICCO	ABRC ABRPR	ABRB ABRPR	RIPT TRIKI	RIP2 BRYDI	RIPS TRIKI	NIGB SAMNI	ABRA ABRPR	RIP1_BRYDI	RIPB_LUFCY	RIP1 CUCFI	MLA VISAL	RIPA LUFCY	RIP2 MOMBA	RIP1 MOMCH	RIP1 TRIAN	RIPG GELMU		RIP1 PHYAM	RIPS PHYAM	RIPP MIRJA			RIP7 SAPOF		RIP6 SAPOF	RIPO_DIACA	RIP2 PHYAM	RIP2_SAPOF	SLTA_BP933		RIP3 MAIZE
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4 5 5 6 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	45

ALIGNMENTS

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STRAND
Min Y., Robertus J.D.,

"Analysis of several key active site residues of ricin A chain by
"Analysis of several key active site residues of ricin A chain by
"Analysis of several key active site residues of ricin A chain by
"The mutagenesis and X-ray crystallography.";

"Entering the single for an implication of several to plant cells. The A chain is responsible for inhibiting protein synthesis through the catalytic inactivation of 60s ribosomal subunits. It acts as a glycosidase that removes a specific adenine residue from an exposed loop of 28s ribosomal RNA. As this loop is involved in the binding of elongation factors, the modified ribosomes are unable to support protein synthesis. The A chain can inactivating them faster than the cell can make new ones. A single A-chain molecule can therefore kill an animal cell. The B chain binds to cell receptors and facilitates the entry into the cell of the A chain, B chains are also responsible for cell agglutination (lectin activity). It binds to beta-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "X-ray structure of recombinant ricin A-chain at 1.8-A resolution."; J. Mol. Biol. 244:410-422(1994).
                                                                     MEDLINE=87165983; PubMed=3558397;
Monfort W., Villafranca J.E., Monzingo A.F., Ernst S.R., Katzin B.,
Rutenber E., Xuong N.H., Hamlin R., Robertus J.D.;
"The three-dimensional structure of ricin at 2.8 A.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96374222; PubMed=8780513; Monzingo A.F., Pascal J.M., Appay P.J., Enrst S.R., Frankel A.B., Monzingo A.F., Pascal J.M., Molina-Svinth M.C., Robertus J.D.; "Structure and activity of an active site substitution of ricin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
MEDLINE=97240820; PubMed=9086280;
Yan X., Hollis T., Svinth M., Day P., Monzingo A.F., Milne G.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95082010; PubMed=7990130;
Weston S.A., Tucker A.D., Thatcher D.R., Derbyshire D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Robertus J.D.; "Structure-based identification of a ricin inhibitor."; J. Mol. Biol. 266:1043-1049(1997).
                                                                                                                                                                                                                                                                                                                                                "Structure of ricin B-chain at 2.5-A resolution.";
                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN. MEDILINE=31352064, PubMed=18818811, KAUTHIN B.J., COllins B.J., Robertus J.D.;
"Structure of rigin A-chain at 2.5 A.";
                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.
MEDLINE=91352005; Pubmed=1881882;
Rutenber E., Robertus J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                       K-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN.
                                                     RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
                                                                                                                          "The three-dimensional structure or
J. Biol. Chem. 262:5398-5403(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochemistry 35:11098-11103(1996).
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                   Toxicon 39:1723-1728(2001).
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   "Ricin.";
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SIMILARITY: Contains 2 ricin B-type lectin domains.
CONFLICTS
ACATION: REF.4 AND REF.5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS
WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3).
DATABASE: NAME=Protein Spotlight;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PSS0231; RICIN B LECTIN; 2.
PROSITE; PS00275; SHIGA RICIN, 1.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; Plyoprotein; Lectin; Signal; 3D-structure.
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N-LINKED (GLCNAC. . .) (IN MINOR FORM).
                                                                       NOTE-Issue 31 of February 2003;
WWW-"http://www.expasy.org/spotlight/articles/sptlt031.html".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /FTIG=CAR 000081.
N-LINKED (GLCNAC. .).
N-LINKED (GLCNAC. .).
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RICIN B-TYPE LECTIN
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LINKER PEPTIDE.
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2-ALPHA.
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InterPro; IPR000772; Ricin_B_lectin.
InterPro; IRR001574; RIP.
Equ. PF00652; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
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PDB, 2AA1, 31.JAN-94.
PDB, 1APG, 31.JAN-94.
PDB, 1FMP, 31.OTN-94.
PDB, 1IFS, 14.JAN-98.
PDB, 1IFT, 14.JAN-98.
PDB, 1IFT, 14.JAN-98.
PDB, 1GT, 14.JAN-98.
PDB, 1GT, 15.OCT-93.
PDB, 1GT, 16.JAN-98.
PDB, 1GBT, 16.JAN-97.
PDB, 1BR5, 02.SEP-98.
PDB, 1BR5, 102.SEP-98.
PDB, 1BR4, 16.JAN-02.
PDB, 1L13, 16.JAN-02.
PDB, 1L14, 16.JAN-02.
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                                                                                                                                                                    122
                                                                                                                                                                                                                                                                           158 YDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICTQMISEAARFQ 217
                                                                                                                                                                                                      98 SNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYTFAFGGN 157
                                                                                                                                                                                                                                                   YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182
                                                                                     62
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Lin T.T.-S., Li S.S.-L.;
Lin T.T.-S., Li S.S.-L.;
Furification and physicochemical properties of ricins and agglutinins from Ricinus communis.";
Eur. J. Biochem. 105:453-459(1980).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-03AN-1988 (Rel. 06, Created)
01-03AN-1988 (Rel. 06, Last sequence update)
01-03AN-1988 (Rel. 06, Last sequence update)
28-FBB-2003 (Rel. 41, Last amnotation update)
Agglutinin precursor (RCA) [Contains: Agglutinin A chain (rRNA N-
Glycosidase) (EC 3.2.2.22); Agglutinin B chain].
Ricinus communis (Castor bean).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                         38 PKOYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=86059449; PubMed=2999130;
Roberts L.M., Lamb F.I., Pappin D.J.C., Lord J.M.;
"The primary sequence of Ricinus communis agglutinin. Comparison with
                                                                                                                                                                SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN
                                                                                   3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                            0; Gaps
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-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
-!- SIMILARITY: Contains 2 ricin B-type lectin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Araki T., Yoshioka Y., Funatsu G.; The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin isolated from large-grain castor bean seeds."; Biochim. Biophys. Acta 872:277-285 (1986).
    Length 576;
                                            0; Indels
  99.1%; Score 1010; DB 1;
100.0%; Pred. No. 1.6e-86;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             564 AA.
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                                                                                                                                                                                                                                                                                                                                183 YIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                218 YIEGEMRTRIRYNRRS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M12089; AAA33869.1; -. EMBL; S40368; AAB22584.1; -.
                                          Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 303-564.
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGL RICCO
P06750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Seed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 YDRLEGL-GGLRENIELGTGPLEDAISALYYYSTCGTGIPTLARSFMVCIQMISEAARFQ 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
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                                                                                                                                                                                                     SMART; SM00458, RICIN 2.
PROSITE; PS50231; RICIN 1.
PROSITE; PS00275; SHIGA_RICIN; 1.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Signal POTENTAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 SNHAELSVILALDVINAYVVGCRAGNSAYFEHPDNQEDAEAITHLFIDVQNSFIFAFGGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 BY SIMILARITY.
306 INTERCHAIN (BY SIMILARITY).
31 BY SIMILARITY.
466 BY SIMILARITY.
509 BY SIMILARITY.
51 BY SIMILARITY.
52 BY SIMILARITY.
52 BY SIMILARITY.
534 N-LINKED (GLCNAC. .) (POTENTIAL).
525 N-LINKED (GLCNAC. .).
537 N-LINKED (GLCNAC. .).
537 N-LINKED (GLCNAC. .).
537 N-LINKED (GLCNAC. .).
537 N-LINKED (GLCNAC. .).
547 N-LINKED (GLCNAC. .).
558 N-LINKED (GLCNAC. .).
568 N-LINKED (GLCNAC. .).
568 N-LINKED (GLCNAC. .).
569 N-LINKED (GLCNAC. .).
569 N-LINKED (GLCNAC. .).
560 N-LINKED (GLCNAC. .).
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P28590;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Abrin-c precursor [Contains: Abrin-c A chain (rRNA N-glycosidase)
RC 3.2.2.22); Abrin-c B chain].
Abrus precatorius (Indian licorice) (Crab's eye).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.3%; Score 920.5; DB 1; Length 564;
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                                                                                                                                                                                                                                                                                                                                                                                                 AGGLUTININ A CHAIN.
LINKER PEPTIDE.
AGGLUTININ B CHAIN.
RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91.8%; Pred. No. 3.5e-78; ive 7; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1-ALPHA.
1-BETA.
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                     HSSP; PO2879; 1BR6.
GlycoSulteDB; P06750; -
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
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                                                                                                                                                                                                  PRINTS; PR00396; SHIGARICIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 91.8
Matches 180; Conservative
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374
404
552
564 AA;
PIR; A24261; RLCSAG.
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DORNAR MARKANA MARKANA
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                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00652; Ricin B_lectin; 6.
Pfam; PF00161; RIP; 1.
PRINTS; PF00196; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS00231; RICIN B_LECTIN; 2.
PROSITE; PS00275; SHIGA RICIN; 1.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I, Fabales, Fabaceae, Papilionoideae, Abreae, Abrus.
NCBI_TaxID=3816,
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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BY SIMILARITY.
ABRIN C A CHAIN (BY SIMILARITY).
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ABRIN C B CHAIN (BY SIMILARITY).
RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
PYRROLIDONE CARBOXYLIC ACID
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2-BETA.
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HSSP; P11140; JARA.
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62817 MW;
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SIGNAL 1 34
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                                                      SEQUENCE FROM N.A.
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448
487
529
198
281
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MOD_RES
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34.7%; Score 353.5; DB 1; Length 562;

Query Match

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                                                                                                                                                                                                                              93 SERESIEVGIDVTNAYVVAYRAGSQSYFL---RDAPASASTYLFPGTQ-RYSLRFDGSYG 148
                                                                                                                                                                                                                                                                            25 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 184
                                                                                                                                                                                  65 HAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYIFAFGGNYD 124
                                                                                                                                   92
                                                                                       64
                                                                                                                       35 ODOVIKFTTEGATSOSYKOFIEALRORLTGG--LIHDIPVLPDFTTVEERNRYITVELSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARE ABRR STANDARD, PRT; 527 AA.

AGE 1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2013 (Rel. 41, Last annotation update)
Abrin-b precursor [Contains: Abrin-b A chain (rRNA N-glycosidase)
(RC 3.2.2.22); Abrin-b B chain)
(RC 3.2.2.22); Abrin-b E chain)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
                                                                                                                                                                                                                                                                                                                      149 DLERWAHQTREEISLGLQALTHAIS---FLRSGASNDEEKARTLIVIIQMASEAARYRYI
                                                                                       5 OYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epecific adenosine on the 28s rRNA.
-!-SUBUNIT. DISULFIDE-LINKED DIMER OF A AND B CHAINS.
-!-DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
-!-SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
INACTIVATING PROTEIN FAMILY TYPE 2 RIP SUBFAMILY.
-!-SIMILARITY: CONTAINS 2 ricin B-type lectin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Seed;

Kimura M., Sumizawa T., Funatsu G.;

The complete amino acid sequences of the B-chains of abrin-a and abrin-b, toxic proteins from the seeds of Abrus precatorius.";

Biosci. Biotechnol. Biochem. 57:166-169(1993).

I- FUNCTION: THE A CHAIN IS REPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOWAL SUBJUITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S. RENA. ARRIN-A. IS MORE TOXIC THAN RICIN.

-I- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FALLIPTES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=91132798; PubMed=8421313; MEDLINE=91132798; PubMed=8421313; Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.; Hung C.-H., Lee the distinct isoabrins determined by cDNA sequencing. Conservation and significance.";
                                           6
       2.4e-25;
                   Pred. No. 2.4e
1; Mismatches
45.5%; ***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Biol. 229:263-267(1993)
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                                           86; Conservative
                                                                                                                                                                                                                                                                                                                                                                       185 EGEMRTRIR 193
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                 Best Local Similarity
Matches 86; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 HABLSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDABAITHLFTDVQNRYTFAFGGNYD 124
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                                                                                                  Pfam; Procci, Procci, Procci, Pram; Prouds, Procci, Pram; Prouds, Procci, Proc
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Y -> D (IN REF. 2).
N -> S (IN REF. 2).
E -> Y (IN REF. 2).
E -> Q (IN REF. 2).
H -> T (IN REF. 2).
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BY SIMILARITY.
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RICIN B-TYPE LECTIN 2.
1-ALPHA.
1-BETA.
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AE -> PQ (IN REF. 2).
S -> N (IN REF. 2).
L -> M (IN REF. 2).
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+ive 22; Mismatches
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2-ALPHA.
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2-GAMMA
                   PIR, S32430, S32430.
HSSP: P11140, 1ARR.
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
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  EMBL; M98345; AAA32625.1;
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RESULT

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MEDLINE=95344383; PubMed=7619070;
MEDLINE=95344383; PubMed=7619070;
MEDLINE=95344383; PubMed=7619070;
MEDLINE=95344383; PubMed=7619070;
"Studies on crystal structures, active-centre geometry and deputinating mechanism of two ribosome-inactivating proteins.";
Biochem. J. 309:285-298 (1995).
-!- FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. IT IS
CAPABLE OF INHIBITING HIV-1 INFECTION AND REPLICATION. IT
INACTIVATES EUKARYOTIC 60S RIBOSOMAL SUBUNITS.
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE I RIP SUBFAMILY.
                                                     01-1007-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ribosome-inactivating protein alpha-trichosanthin precursor
(rRNA N-glycosidase) (EC 3.2.2.2) (Alpha-TCS).
Trichosanthes Airilowii (Mongolian snake-gourd).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chow T., Feldman R.A., Lovett M., Piatak M.;
"Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a "type I ribosome-inactivating protein.";
J. Biol. Chem. 265:8670-8674(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Tuberous root;
Wang Y., Qian R.Q., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X.,
Tian G.Y., Ni C.Z.;
"Scientific evaluation of Tian Hua Fen (THF): history, chemistry and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Maximowicz; TISSUE=Tuberous root; MEDINE=90256789; PubMed=234139; Collinne E.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.R., Wu P., Hwang K., Piatak M.; Popresti M., Stone K.L., Williams K.R., Mu P., Hwang K., Piatak M.; Gardence of alpha-trichosanthin and molecular models for abrin A-chain and alpha-trichosanthin."; J. Biol. Chem. 265:8665-8669(1990).
                                                                                                                                                                                                                                                                                               STRAIN-Maximowicz;
MRDINIR-91153657; PubMed=1999291;
Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;
"Cloning of trichoeanthin cDNA and its expression in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94344957; PubMed=8066085; Zhou F., Pan K.; M. Z., Chen M., Lin Y., Pan K.; Structure of trichosanthin at 1.88-A resolution."; Proteins 19:4-13(1994).
  289 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pure Appl. Chem. 58:789-798(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=Maximowicz; TISSUE=Leaf;
MEDLINE=90256790; Pubmed=2341400;
                                         Created)
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                    Gene 97:267-272(1991).
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                                                InterPro; IRRO11574; RIP.
Prim: PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGARICIN.
Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
Prain; Signal; 3D-structure.
SIGNAL
24 270 RIBOSOME-INACTIVATING PROTEIN ALPHA-
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| MISSING (IN REF. 4).
| MISSING (IN REF. 4).
| V -> VDACLPENAVL (IN REF. 4).
| XI -> GL (IN REF. 4).
| X -> GL (IN REF. 4).
| WS -> LWL (IN REF. 4).
| WS -> LWL (IN REF. 4).
| WS -> LWL (IN REF. 5).
| WS -> LWL (IN REF. 5).
| WISSING (IN REF. 2).
| MISSING (IN REF. 2).
| MISSING (IN REF. 2).
                                                                                      TRICHOSANTHIN.
MISSING IN MATURE PROTEIN
                                                                                               SIMILARITY.
send an email to license@isb-sib.ch).
        EMBL; M34858; AAA34207.1; -.
                 PIR, JT0566; RLTZT.
PDB; IMRJ, OT-FEB-95.
PDB; IMRK, 07-FEB-95.
PDB; ITCS; 10-JUL-95.
PDB; 1J4G; 28-JAN-03.
PDB; 1NLI; 21-JAN-03.
PDB; 1QD2; 24-APR-00.
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                                                                                                                                                                                                                                                                                                                                                                                 69 SVTLALDVTNAYVVGYRACNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 127
                                                                                                                                                                                                                                                                                                                                                                                                                  82 IISVAIDVTNVYIMGYRAGDISYFF---NEASATEAAKYVFKDAMRKVTLPYSGNYERLQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28 QLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 68
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Bioconj. Chem. 5:423-429(1994).
-!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S FRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
-!- TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIP2 BRYDI STANDARD; PRT; 282 AA.

P98184: 0958J0;

16-027-2001 (Rel. 40, Last sequence update)

26-FEB-2003 (Rel. 41, Last annotation update)

26-FEB-2003 (Rel. 41, Last annotation update)

Ribosome-inactivating protein bryodin II precursor (rRNA N-glycosidase) (EC 3.2.2.2) (BD2).

Bryonia dioica (Red bryony).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Bryonia.
                                                                                                                                                                                                                                                                                                    12; Gaps
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Siegall C.B., Gawlak S.L., Marquardt H.;
"Bryodin 2 a ribosome-inactivating protein isolated from the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Characterization of ribosome-inactivating proteins isolated from Bryonia dioica and their utility as carcinoma-reactive
                                                                                                                                          Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Root;
MEDLINE=95151812; PubMed=7849072;
Siegall C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B.,
Marquardt H.;
                                                                                                                                                                                                    46; Mismatches 54; Indels
                                                                                      31676 MW; 5CE09BB630575BB9 CRC64;
                                                                                                                                             33.6%; Score 342; DB 1; 39.5%; Pred. No. 1.2e-24;
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HSSP; P09989; 1MRJ.
                                                                                                                                                                                                       73; Conservative
260 2
263 2
266 2
289 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 22-42.
                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 MRTRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 IGKRV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bryonia dioica."
                                                                                      SEQUENCE
                                                                                                                                             Query Match
Best Local
STRAND
STRAND
TURN
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                                                                                                                                                                                                           Matches
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ACT SITE
SEQUENCE
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                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                      SIGNAL
                                                                                                                                                                                             PROPEP
                                                                                                                                                                   CHAIN
                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                              69 LSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLE 127
                                                                                                                                                                                                                                                                                                         81 ESVTVALDVVNVYVVAYRAGNTAYFL---ADASTEANNVLFAGI-NHVRLPYGGNYDGLE 136
                                                                                                                                                                                                                        9 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPN-RVGLPINQRFILVELSNHAE 67
                                                                                                                                                                                                                                                  24 INFSLIGATGATYKTFIRNLRTKLTVGTPRVYDİPVLRNAAAGL---ARFQLVTLTNYNG 80
                                                                                                                                                                                                                                                                                                                                     128 QLAGNL-RENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIE 185
                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97356562; PubMed=9212998; Mizukami H., Idda K., Kondo T., Ogihara Y.; Idda K., Kondo T., Ogihara Y.; Idda M. Addo T., Deloning and bacterial expression of a gene encoding ribosome-inactivating proteins, karasurin-A and karasurin-C, from Trichosanthes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chem. Pharm. Bull. 39:1244-1249(1991).
-!- FUNCTION: ABORTION-INDUCING PROTEIN. IT INACTIVATES BUKARYOTIC
-!- GOS RIBOSOMAL SUBUNITS.
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
                                                                                              RIBOSOME-INACTIVATING PROTEIN BRYODIN II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I; Cucurbitales, Cucurbitaceae, Trichosanthes.
                                                                                                                                                                                             13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specific adenosine on the 288 FRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.
                                                                                                                      25 25 N-LINKED (GLCNAC. . .) (POTENTIAL) 282 AA; 30754 MW; C52BE2F6A873769C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92005921; PubMed=1914000;
Toyokawa S., Takeda T., Kato Y., Wakabayashi K., Ogihara Y.;
"The complete amino acid sequence of an abortifacient protein,
           Pfam, PF00161; RIP; 1.
PRINTS; PR0396; SHIGARICIN.
PROSITE; PS00775; SHIGARICIN; 1.
Plant defense; Protein Synthesis inhibitor; Hydrolase; Toxin;
                                                                                                                                                                   DB 1; Length 282;
                                                                                                                                                      33.5%; Score 341.5; DB 1; Lengua. 48.0%; Pred. No. 1.3e-24; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR 1992 (Rel. 21, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein karasurin precursor (rRNA N-glycosidase) (EC 3.2.2.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trichosanthes kirilowii (Mongolian snake-gourd)
                                                                                                         BY SIMILARITY.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                    289 AA.
                                                                 Multigene family; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kirilowii var. japonica.";
Biol. Pharm. Bull. 20:711-713(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                             Conservative
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                 21
282
183
25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEOUENCE OF 24-270.
                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Root tuber;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3677;
                                                                                                          183
                                                                                                                                                                                            96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     karasurin."
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                                                                                                         ACT SITE
                                                                                                                                       SEQUENCE
                                                                                SIGNAL
                                                                                              CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 INFITAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96215449; PubMed=8647092;
Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.;
Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.;
"Characterization and molecular cloning of Sambucus nigra agglutinin (nigrin b), a GalNAc-specific type-2 ribosome-inactivating protein Erom the bark of elderberry (Sambucus nigra).";
Eur. J. Biochem. 237:505-513(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1993 (Rel. 27, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nigrin b precursor (Agglutinin V) (SNAV) [Contains: Nigrin b A chain (rRNA N-glycosidase) (EC 3.2.22); Nigrin b B chain].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDILINE=94003077; PubMed=8400135;
Girbes T., Citores L., Ferreras J.M., Rojo M.A., Iglesias R.,
Munoz R., Arias F.J., Calonge M., Garcia J.K., Mendez E.;
"Isolation and partial characterization of nigrin b, a non-toxic
novel type 2 ribosome-inactivating protein from the bark of Sambucus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nigra L.";
Plant Mol. Biol. 22:1181-1186(1993).
-!- FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAMMALIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, campanulids, Dipsacales, Adoxaceae, Sambucus.
                                                                                                                                                          PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.2%; Score 338; DB 1; Length 289; 40.0%; Pred. No. 2.9e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53; Indels
                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
883D3E3242887B26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                     REMOVED IN MATURE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                563 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46; Mismatches
                                                                                                                                                                                                                                                                                                         KARASURIN-C.
KARASURIN-A.
                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sambucus nigra (European elder).
                                                                                                                                                                                                                                                                                                   22 270 KAF
24 270 KAF
271 289 REI
183 183 BY
289 AA; 31704 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 26-49 AND 298-321.
EMBL; AB000666; BAA21786.1;
                    PIR; JC5606; JC5606.
PIR; JU0393; JU0393.
HSSP; P09989; JMRJ.
InterPro; IPRO01574; RIP.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P33183; P33184; P93542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 MRTRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194 IGKRV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4202;
                                                                                                                                                                                                                                                       loxin; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Bark;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIGB SAMNI
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87
PROTEIN SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL PROTEIN SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS. THROGGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBVINITS BY REMOVING ADENIUS FROM POSITION 4,324 OF 28 SRNA. THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT PRILLITATES THE
                                                                                                                                                                            -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00652; Ricin B lectin; 6.
Pfam; PF00161; RIP; I.
PRINTS; PR00396; SHTGARICIN.
SMART; SMO0458; RICIN; 2.
PROSITE; PS00275; SHIGA RICIN; 1.
PROSITE; PS50231; RICIN B LECTIN; 2.
PROSITE; PS50231; RICIN B LECTIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61; Indels 15; Gaps
                                                                                                                                                                                                                                                          -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
-!- SIMILARITY: Contains 2 ricin B-type lectin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL) .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 330.5; DB 1; Length 563; Pred. No. 3.3e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERCHAIN (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIGRIN B A CHAIN.
NIGRIN B B CHAIN.
RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC. . .)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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1-BETA.
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2-ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2-GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2-BETA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; S37382; S37382.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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434
316
357
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signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75;
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     SOLUTION STATEMENT STATEME
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
142 DNLETAANTRRESIELGPSPLDGAITSLYHGD-----SVARSLLVVIQMVSEAARFRY 194
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                                                                                                                                                                                                                                                                                                                       Abrus precatorius (Indian licorice) (Crab's eye).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Funatsu G., Taguchi Y., Kamenosono M., Yanaka M.;
"The complete amino acid sequence of the A-chain of abrin-a, a toxic protein from the seeds of Abrus precedtorius.";
Agric. Biol. Chem. 52:1095-1097(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at specific adenosine on the 28S rRNA.
-!- SUBGUILT: DISCULFIDE-LINKED DIMBER OF AND B CHAINS.
-!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95333188; PubMed=7608980;
Tahirov T.H., Lu T.-H., Liaw Y.-C., Chen Y.-L., Lin J.-X.;
Tahirov T.H., Lu abrin-a t 2.14 A.";
J. Mol. Biol. 250:354-367(1995)
-:- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOWAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RRNA.
                                                                                                                                                                                                P11140; P28589;
01-JUL-1889 (Rel. 11, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Abrin-a precursor [Contains: Abrin-a A chain (rRNA N-glycosidase)
(EC 3.2.2.2); Abrin-a B chain].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.; "Primary structure of three distinct isoabrins determined by cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Evensen G., Mathiesen A., Sundan A.; "Direct molecular cloning and expression of two distinct abrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABRIN-A IS MORE TOXIC THAN RICIN.
FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
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Chen Y.-L., Chow L.-P., Tsugita A., Lin J.-Y.;
"The complete primary structure of abrin-a B chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequencing. Conservation and significance.";
J. Mol. Biol. 229:263-267(1993).
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                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93132798; PubMed=8421313;
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                                      184 IEGEMRTRIR 193
                                                                            195 IEQEVRRSLQ 204
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                                 EMBL; W98344; AAA32624.1; ALT_INIT.

R EMBL; X54872; -; NOT_ANNOTATED_CDS.

PIR; 532492; TZLSA.

PIR; 532492; TZLSA.

PIR; 532492; TZLSA.

R EDB; 1ABR; 07-FEB-95.

RINTERPRO; IPRO00772; Ricin B lectin.

R Pfam; PF00652; Ricin B lectin; 6.

R Ffam; PF00652; Ricin B lectin; 6.

R Ffam; PF00396; SHIGARICIN.

R RAWAT; SM00458; RICIN; 1.

R RAWAT; SM0458; RICIN; 1.

R ROSITE; PS00275; SHIGARICIN; 1.

PROSITE; PS00275; SHIGARICIN; 1.

R PROSITE; PS01275; RICIN B LECTIN; 2.

R CHAIN

CHAIN

251 ARBINA BETINE.

PT DOMAIN

273 400 RICIN B-TYPE LECTIN 1.
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BY SIMILARITY.
BY SIMILARITY.
FYROLIDONE CARBOXYLIC ACID.
N-LINKED (GLCNAC. . .).
MISSING (ILN REF. 2).
N -> Y (IN REF. 4).
M -> L (IN REF. 4).
T -> P (IN REF. 4).
V -> L (IN REF. 4).
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INTERCHAIN (BY SIMILARITY)
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1-GAMMA.
2-ALPHA.
2-BETA.
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69 SVTLALDVTNAYVVGYRAGNSAYFFH--PDNQEDABALTHLFTDVQNRYTFAFGGNYDRL 126
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match 32.3%; Score 329.5; DB 1; Length 528; Best Local Similarity 42.8%; Pred. No. 3.8e-23; Matches 80; Conservative 28; Mismatches 66; Indels 13
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127 EQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG 186
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-!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
PROTEIN SYNTHESIS IN ANIMAL CELLS.
-!- CATALYIIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S FRNA.
-!- PTM: APPEARS TO UNDERGO PROTEOLYTIC CLEAVAGE IN THE C-TERMINAL TO
                                                                                                                                                                                                                                                                P33185; Q9S819;
01-0CT-1993 (Rel. 27, Created)
16-0CT-2001 (Rel. 27, Created)
18-0CT-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein bryodin I precursor (rRNA N-glycosidase)
Rronia dioica (Red bryony).
Bryonia dioica (Red bryony).
Bryonyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyjedons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Bryonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular, biological, and preliminary structural analysis of recombinant bryodin 1, a ribosome-inactivating protein from the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRODUCE A SHORTER PROTEIN.

BIOTECHNOLOGY: Especially useful as immunotoxin for pharmacological applications as it has low toxicity in rats and mice but is potent once inside target cells.

SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Montecucchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of ribosome-inactivating proteins isolated from Bryonia dioica and their utility as carcinoma-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isegali C.B.;
Cloning and expression of a gene encoding bryodin 1 from Bryonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Leaf;
MEDILNE=97228081; PubMed=9115985;
Gawlak S.L., Neubauer M., Klei H.E., Chang C.Y.Y., Einspahr H.M.,
Siegall C.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "N" terminal sequence of some ribosome-inactivating proteins."; Int. J. Pept. Protein Res. 33:263-267(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Siegall C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent number US5541110, 30-JUL-1996
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MEDLINE=89326691; PubMed=2753596;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochemistry 36:3095-3103(1997).
STANDARD;
                                                                                                                         187 EMRTRIR 193
                                                                                                                                                           174 RVRVSIQ 180
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between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                       RIBOSOME-INACTIVATING PROTEIN BRYODIN I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
E-XF. REDUCES ACTIVITY 10-FOLD.
RSSIS -> LRHXI (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                            Pfam; PF00161; RIP; 1. PRIVIN: PROSITE; PS00396; RIFGARICIN. PROSITE; PS00275; SHIGARICIN: 1. PLOSITE; PS00275; SHIGARICIN: 1. Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; 310-structure; Multigene family; Glycoprotein; Signal. 1. 23
                                                                                                                                                                                                                                                                                                                                                                                                                                    30.6%; Score 312; DB 1; Length 290; 37.3%; Pred. No. 7.7e-22; Live 46; Mismatches 58; Indels 1
                                                                                                             MISSING IN MATURE PROTEIN.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                         31788 MW; E966CD9C031A42DB CRC64;
                                        EMBL; I24020; -; NOT_ANNOTATED_CDS.
PIR; S16491.
PDB; 18RY; 04-MAR-98.
InterPro; IPRO01S74; RIP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 AITMAIDVTNVYIMGYLVNSTSYF---ANESDAKLASQYVFKGSTLVTIPYSGNYERLON 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       129 LAGNLRENIELGNGPLEEAISALYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 188
                                                69 SVILLALDVINAYVVGYRAGNSAYFFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 127
                                                                 82 IISVAVDVINVYIMGYLAGDVSYFF---NEASATEAAKFVFKDAKKKVTLPYSGNYERLQ 138
                                                                                                .28 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 187
                                                                                                               9
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9 INFITAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 68
              Islam M.R., Hirayama H., Funatsu G.;
"Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from sponge gourd (Luffa cylindrica) seeds.";
Agric. Biol. Chem. 55:229-338(1991).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
-! TYPE I RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I; Cucurbitales, Cucurbitaceae, Iuffa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPRO01574; RIP.
Interpro; IPRO01574; RIP.
PRIM: PRO0161; RIP. 1.
PRIMTS; PRO0396; SHIGARICIN.
PROSITE; PRO02575; SHIGARICIN, 1.
PROSITE; PRO02575; SHIGARICIN, 1.
Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.5%; Score 300.5; DB 1; Length 250; 34.2%; Pred. No. 7.6e-21; live 48; Mismatches 64; Indels 11.
                                                                                                                                                                                                                                                                01-AUG-1991 (Rel. 19, Created)
1-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein luffin-B (rRNA N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27293 MW; F01A8DC8A1078700 CRC64;
                                                                                                                                                                                                                                                                                                                                 Luffa cylindrica (Smooth loofah) (Sponge gourd)
                                                                                                                                                                                                                                           250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91248488; PubMed=136866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.2%;
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                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 RTRIRYN 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; JN0108; JN0108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P16094; 1AHC
                                                                                                                                                  188 MRTRI 192
                                                                                                                                                                    : |:
194 IGKRV 198
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160
                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Seed;
                                                                                                                                                                                                                                          RIPB LUFCY
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 OLAGNLRENIELGNGPLEEAISALYYYSTGGTOLPTLARSFIICIOMISEAARFOYIEGE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant Biotechnol. 17:337-340(2000).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28s rRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 VKFSLLGSNHKSYSKFITSMRNALPNAGDI-YNIPLLVPSISG---SRRYILMQLSNYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVL-PNRVGLPINQRFILVELSNHAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 LSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLE
                                                                                                                                                                                                            Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosida I, Cucurbitales, Cucurbitaceae, Cucumis.
NCBI_TaxID=131071,
                                                                                                                                         Putative ribosome-inactivating protein precursor (rRNA N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUTATIVE RIBOSOME-INACTIVATING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
PRNUTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGAR ALCIN; 1.
PROSITE; PS00275; SHIGAR ALCIN; 1.
Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29.1%; Score 296.5; DB 1; Length 286; 34.4%; Pred. No. 2.1e-20; tive 47; Mismatches 64; Indels 13.
                                                                                                                                                                                                                                                                                                                                                                           1 21 POTENTIAL.
22 286 PUTATIVE RIBOSOME-INACTIVA
185 185 BY SIMILARITY.
103 103 N-LINKED (GLCNAC. .) (PO
110 110 N-LINKED (GLCNAC. .) (PO
252 252 N-LINKED (GLCNAC. .) (PO
286 AA; 31771 MW; 4EFD4966E604DA41 CRC64;
                                                                               (Rel. 40, Last sequence update) (Rel. 41, Last annotation update)
286 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB045560; BAB19677.1; -.
HSSP; P16094; 1AHC.
                                                       16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ilarity 34.4%;
Conservative 4
STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                   Cucumis figarei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Toxin; Signal SIGNAL
                                                                                     16-OCT-2001
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65;
CUCFI
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CARBOHYD
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                           O9FRX4;
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131 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARF-----Q 182

8

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"Complete amino acid sequence of the A chain of mistletoe lectin I.";
PEBS Lett. 399-153-157(1996).
-!- FEBS Lett. 399-153-157(1996).
-!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
SYNTHEELS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RENA. THE
B CHAIN BINDS TO CELL RECEPTORS AND PROBABLY FACILITATES THE ENTRY
INTO THE CELL OF THE A CHAIN; B CHAINS ARE ALSO RESPONSIBLE FOR
CELL AGGLUTINATION (LECTIN ACTIVITY).
-!- CATALYTIC ACTIVITY: EndobyAcolysis of the N-glycosidic bond at one
specific adenosine on the 28S TRNA.
-!- SUBUNIT: Disulfide-linked dimer of A and B chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHARMACEUTICAL: Due to its immunomodulative effects it is being studied in clinical trials in cancer patients as it may slow the growth of cancer cells and be an effective treatment for solid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- MISCELLANEOUS: TWO ISOFORMS OF MLA EXIST; GLYCOSYLATED FORM MLA AND NON-GLYCOSYLATED FORM MLA'.
                                          15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Beta-galactoside specific lectin I A chain (MLA) (ML-I A) (rrnA N-glycosidase) (EC 3.2.2.2)
Viscum album (European mistletoe).
Viscum album (European mistletoe).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soler M.H., Stoeva S., Schwamborn C., Wilhelm S., Stiefel T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> S (IN MLA').
53BAF98D3E0FFE67 CRC64;
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V -> M (IN MLA').
V -> M (IN MLA').
V -> ST (IN MLA').
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.1%; Score 286; DB 1; 38.4%; Pred. No. 1.7e-19; iive 36; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IN MLA')
 254 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 O M X
                                                                                                                                                                                                                  STRAIN=Subsp. album;
MEDLINE=97134581; PubMed=8980141;
                                                                                                                                                        Santalales; Santalaceae; Viscum.
                               15-DEC-1998 (Rel. 37, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28478 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR, PD0018, PD0018.
HSSP, P11140, 1ABR.
InterPro, IPR001574, RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE 2 RIP SUBFAMILY.
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 ;
254 AA;
                                                                                                                                                                     NCBI_TaxID=3972;
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112
15
66
112
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MLA VISAL
P81446;
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71 TLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 130

9 THOTTGEEYFRFITLLRDYVSSGS-FSNEIPLL-ROSTIPVSDAORFVLVELTNOGODSV 13 TAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPIN--QRFILVELSNHAELSV

70 99

38; Gaps

Conservative

Local Similarity es 81; Conserv

Matches

ð q δ

Length 254; 56; Indels

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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 VRFSLSGSSSTSYSKFIGDLRKALPSNGTVTNITLLSSASGA---SRYTLMTLSNYDGK 78
                                                                                                                                                                                                                                                                                                                                                                                                                        Kataoka J., Habuka N., Miyano M., Masuta C., Koiwai A.;
"Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-
inactivating protein from Luffa cylindrica.";
Plant Mol. Biol. 18:1199-1202(1992).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28s rRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.
                                                                                                                                                           O'DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 41, Last annotation update)
80-FBB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein luffin-alpha precursor (rRNA N-glycosidase) (EC 3.2.2.2)
10.4ffa cylindrica (Smooth loofah) (Sponge gourd).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida I; Cucurbitales; Cucurbitaceae; Luffa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIBOSOME-INACTIVATING PROTEIN LUFFIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.9%; Score 284.5; DB 1; Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 2.7e-19;
----GEMRTRIRYN 195
                                  179 YİNSGASFLPDVYMLELETSWĞQQSTQVQHS 209
                                                                                                                              277 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=92288316; PubMed=1600156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30212 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X62371; CAA44229.1; ...
PIR; S22494; S22494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P16094; 1AHC.
InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
183 YIE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63; Conservative
                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      WCBI_TaxID=3670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Poxin, Signal
                                                                                                                            RIPA LUFCY Q00465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                            RIPA LUFCY
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                                                                                           RESULT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n,
                    62 LISNHAELSVTLALDVTNAXVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 LAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 NYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ortigao M., Better M.;
"Momordin II, a ribosome inactivating protein from Momordica
balsamina, is homologome inactivating proteins.";
Nucleic Acids Res. 20:4662-4662(1992).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE I RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                     Momordica balsamina (Bitter gourd) (Balsam pear).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; Rosidae,
eurosids I; Cucurbitales, Cucurbitaceae, Momordica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
Plant defense; Protein Synthesis inhibitor; Hydrolase; Toxin; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIBOSOME-INACTIVATING PROTEIN MOMORDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.6%; Score 281; DB 1; Length 286; 35.1%; Pred. No. 5.9e-19; trive 42; Mismatches 72; Indels
                                                                                                                                                                                                                             01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ribosome-inactivating protein womordin II precursor (rRNA N-glycosidase) (EC 3.2.2.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3B89FF1AE6B25986 CRC64;
                                                                                                                                                                                               286 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY
                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93027170; PubMed=1408771;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z12175; CAA78166.1; -. PIR; S25560; S25560.
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PDB; 1CF5; 07-JUN-99.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68; Conservative
                                                                                                                                                                                               STANDARD;
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286
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                                                                      189 RTRIRYNR 196
                                                                                                      191 IERISKNQ 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 68; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 24
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                                                                                                                                                                                              RIP2 MOMBA
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Search completed: February 10, 2004, 16:23:24 Job time : 6.60489 secs
                                            182 QYIEGEMRTRIRYN 195
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 10, 2004, 16:17:00 ; Search time 26.4196 Seconds Run on:

(without alignments) 1933.961 Million cell updates/sec

US-10-083-336A-7 1019 Title: Perfect score:

1 MVPKQYPIINFTTAGATVQS......ARFQYIEGEMRTRIRYNRRS 198 Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

830525 Total number of hits satisfying chosen parameters:

830525 seqs, 258052604 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPIREMBL 23:* Database

sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mn:*
sp_organelle:*
sp_phage:* sp_vertebrate:*
sp_unclassified:* sp_rvirus:* sp_bacteriap:* sp_archea:* sp_bacteria:* sp_plant:*
sp_rodent:*
sp_virus:* sp_archeap:* 9: 10: 11: 12:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	tion	Q41174 ricinus com	cinnamomum			cinnamomum		sampacas eb	abrus preca			trichosanth					
	Description	041174	Q94bw3	Q94bw4	Q94bw5	Q9£v22	004367	Q9avr2	90900	Q94ke4	Q9lre3	041216	038760	094582	Q8qt32	038761	081007
SUMMERTES	ΠD	041174	Q94BW3	Q94BW4	Q94BW5	Q9FV22	004367	Q9AVR2	206076	Q94KE4	Q9LRE3	041216	Q38760	Q945S2	Q8GT32	Q38761	OSLPV7
		101	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
	* Query Match Length DB	541	580	580	581	549	563	564	528	289	247	289	252	563	563	252	270
	% Query Match	98.86	39.4	39.0	39.0	38.8	34.4	34.1	33.8	33.4	33.2	33.2	33.0	32.4	32.4	32.3	31.8
	Score	1007	401.5	397.5	397.5	395.5	350.5	347.5	344.5	340	338	338	336.5	330.5	330.5	329.5	324
	Result No.		7	æ	4	Ŋ	9	7	σο	σ	10	11	12	13	14	15	16

Q96236 abrus preca Q96237 abrus preca O04071 sambucus ni Q41611 trichosanth Q96235 abrus preca	abrus sambuc luffa sambuc			sambu viscu momor viscu iris	Q8w2e7 iris hollan O04356 iris hollan Q9m653 polygonatum Q8gzn9 euphorbia s Q8vyu0 jatropha cu Q8w2e8 iris hollan
Q96236. Q96237 O04071 Q41611 Q96235	Q9M6E9 004072 Q00980 Q41358	Q8LKQ5 O22415 Q9M654 Q8LKQ4	QBLKQ6 Q9FSH2 Q9FUV7 QBS452 QBW243	P93543 Q8RXH6 Q41257 Q8RXH7 O04358	Q8W2E7 Q04356 Q9M653 Q8GZN9 Q8VYU0 Q8W2E8
100	10110	2222	00000	20000	100000
251 251 565 270 251	547 566 278 570	249 570 604 251	254 264 293 593	0 E B 4 0	592 603 299 573
31.7 31.6 31.3 31.1	30.9 30.5 28.6				2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2. 2
7 75	314.5 310.5 307.5 291	285 285 283.5 283	282 280 279 278 278	277 275 274 273	270 268 266.5 262.5 261 261
17 19 20 21 21	22 22 24 25	26 27 29	33 33 33 44	33 33 33 33 33 33	4 4 4 4 4 0 4 2 4 4 4 7 4 5 5

ALIGNMENTS

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MEDLINE-9233837; PubMed=1633311;

MEDLINE-9233837; PubMed=1633311;

Molecular cloning of ricin.";

Largeted Diagn. Ther 7:81-97(1992)

- CATALYNIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADDROSINE ON THE 288 RRNA.

-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

REMBL, $40469; JBR6.

RISSP, P02879; JBR6.

RICEPPO; IPR00172; Ricin B lectin.

InterPro; IPR001400; Somatotropin.

RICEPPO; RICHOLS, Ricin B lectin; 6.

Péam; PF00652; Ricin B lectin; 6.
                                                                                                                                 Ricinus communis (Castor bean).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1
60281 MW; 2B7B2CDEF1F2E9D9 CRC64;
                                        041174;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAV-2003 (TrEMBLrel. 23, Last amortation update)
Proricin A chain (EC 3.2.2.22) (rRNA N-glycosidase)
                              541 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS5021; RICIN B LECTIN; 2. PROSITE; PS00275; SHIGA RICIN; 1. PROSITE; PS00338; SOMATOTROPIN_2; 1.
                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00396; SHIGARICIN. SMART; SM00458; RICIN; 2.
                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           541 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; Toxin.
                                                                                                                          (Fragment).
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SEQUENCE
                             041174
RESULT 1
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us-10-083-336a-7.rspt

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 RLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 DLERVAGERREEIILGMDPLENAISALMISNL--NQQRALARSLIVVIQMVAEAVRFRFI 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 182
                                                                                                                                                                                                                                                                                                    63 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 YDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICTOMISEAARFO 182
                                                                                                                                                                                                                                                                                                                                                                          63 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64
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                                                                                                                                                    3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 62
                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                patterns.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AY039803; AAK82460.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. Yang O., Gong Z.Z., Liu W.Y.; Yang O., Gong Z.Z., Liu W.Y.; "Modecular cloning of three type 2 RIP (ribosome-inactivating protein) genes encoding cinnamomin proteins and study of their expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN-
                                                                                                                                                                                                          3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHDIPVLPNRVGLPINQRFILVEL
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Type 2 ribosome-inactivating protein cinnamonin III precursor (EC 3.2.2.2.2) (FRNA N-glycosidase). Cinnamomum camphora (Camphor tree). Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE 2 RIBOSOME-INACTIVATING PROTEIN CINNAMOMIN III.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum
NCBL_TaxID=13429;
Score 1007; DB 10; Length 541;
Pred. No. 1.7e-86;
1; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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SMART; SW00458; RICIN; 2.
PR0SITE; PS50231; RICIN_B_LECTIN; 2.
Hydrolase; Signal; Toxin.
32 POTENTI!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP. _____
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 YIEGEMRTRIRYNRRS 198
Query Match
Best Local Similarity 99.5%;
Matches 195; Conservative
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65 HAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 124
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                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A. Yang Q., Gong Z.Z., Liu W.Y.;
"Molecular cloning of three type 2 RIP (ribosome-inactivating protein) genes encoding cinnamomin proteins and study of their expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 YQTVTFTTXNATKTSYTQFIEALRAQLASGEE-PHGIPVMRDGSTVPDSKRFILVELSNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                    Type 2 ribosome-inactivating protein cinnamomin II precursor (EC 3.2.2.2) (rRNA N-glycosidase). (finamomum camphora (Camphor tree). Eukaryor, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum. NCBI_TaxID=13429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE 2 RIBOSOME-INACTIVATING PROTEIN CINNAMOMIN II. 37E4289ECCEOCEFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.0%; Score 397.5; DB 10; Length 580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
1-Mar 2 ribosome-inactivating protein cinnamomin I precursor (EC 3.2.2.22) (TRNA N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58; Indels
                                                                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Pred. No. 6.7e-29; 30; Mismatches 58
                                                                                                 580 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN_B_LECTIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam, PF00652; Ricin B_lectin, 6.
Pfam, PF00161; RIP; 1.
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                                                                                                 PRELIMINARY;
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185 EGEMRTRI 192
                           207 EYRVRESI 214
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Q94BW5;
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                                                                                                 094BW4
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                                                                    RESULT 3
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InterPro; IPR000772; Ricin_B_lectin.
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563 AA;
                                                                                            Hydrolase; Toxin.
                                                                                                      NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                     6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN- 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 YQTVIFITKNATKISYIQFIEALRAQLASGEE-PHGIPVMRERSTVPDSKRFILVELSNW 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XIE L., Liu W.-Y., Wang E.-D.;
"Molecular cloning of cinnamomin A-, B-chain and the expression,
"molecular cloning of cinnamomin A-, B-chain and the A-chain.";
purification, characterization and mutagenesis of the A-chain.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL, AR255548; AAF68978.2; --
HSSP; P02879; 2AAI.
                                                                                                                                Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
                                                             SEQUENCE FROM N.A.

Yang Q., Gong Z.Z., Liu W.Y.;

"Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
genes encoding cinnamomin proteins and study of their expression
                                                                                                                                                                                                                                                                                                                                                                                                           7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-077-2002 (TrEMBLrel. 22, Last amnotation update)
Type II ribosome-inactivating protein cinnamomin (EC 3.3.2.22) (rRNA
                                                                                                                                                                  -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

EMBL; AX03801; AAK82458.1; -1
InterPro; IPR000773; Ricin B lectin.

Pfam; PF00552; Ricin B lectin; 5.

Pfam; PF00552; Ricin B lectin; 5.

Pfam; PR00154; RICin B lectin; 5.

Pfam; PR00595; SHIGARICIN.

SMART; SM00458; RICIN; 2.
           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Laurales, Lauraceae, Cinnamomum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Laurales, Lauraceae, Cinnamomum.
                                                                                                                                                                                                                                                                                                                     TYPE 2 RIBOSOME-INACTIVATING PROTEIN CINNAMOMIN I.
                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 581;
                                                                                                                                                                                                                                                                                                                                                                              39.0%; Score 397.5; DB 10; Length 50.0%; Pred. No. 6.7e-29; tive 27; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                     6E8F5FB8FBA3D196 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 549 AA.
                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                  PROSITE; PS50231; RICIN B LECTIN; 2.
Hydrolase; Signal; Toxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cinnamomum camphora (Camphor tree)
Eukaryota; Viridiplantae; Streptop
Cinnamomum camphora (Camphor tree)
                                                                                                                                                                                                                                                                                                                                                      581 AA; 64215 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-glycosidase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                        94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 EGEMRTRI 192
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                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                   NCBI_TaxID=13429;
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                                                                                                                      patterns
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Best Local S
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 DLEGVAGERREEILLGMDPLENAISALWISNL--NQORALARSLIVVIQWVAEAVRFRFI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 HAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YOTVTFTTKKATKTSYTQFIEALRAQLASGEE-PHGIPVMRERSTVPDSKRFILVELSNW 59
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-! - SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. BMBI; U76524; AAC15886.1; - - HSSP; PO2879; 2AAI.
                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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563 RIBOSOME INACTIVATING PROTEIN, B CHAIN.
62336 MW, 3ED2B6C08E796205 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, campanulids, Dipsacales, Adoxaceae, Sambucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Van Damme E.J., Roy S., Barre A., Rouge P., Van Leuven F., Peumans W.J., "The major elderberry (Sambucus nigra) fruit protein is a lectin derived from a truncated type 2 ribosome-inactivating protein."; Plant J. 12:1251-1260(1997).
                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                               38.8%; Score 395.5; DB 10; Length 549; 50.0%; Pred. No. 9.6e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-UUL-1997 (TrEMBLrel. 04, Created)
01-UUL-1997 (TrEMBLrel. 04, Last sequence update)
01-UUL-1997 (TrEMBLrel. 22, Last annotation update)
Ribosome inactivating protein precursor (EC 3.2.2.22) (rRNA N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                549 AA; 60648 MW; 02607FE607CA44B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                             60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                563 AA.
                                                                                                                                                                                                                                                                                                                                                                             94; Conservative 27; Mismatches
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SMART; SMO0458; RICIN; 2.
PROSITE; PS50231; RICIN; 2.
PROSITE; PS00275; SHIGA_RICIN; 1.
Hydrolase; Signal; Toxin.
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InterPro, IPR001574; RIP.
Ban; PP00162; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; I.
                                                                                     PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN_B_LECTIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=98112023; PubMed=9450339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sambucus nigra (European elder).
                       Pfam; PF00652; Ricin B lectin;
Pfam; PF00161; RIP; I.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 EGEMRTRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EYRVRGSI 182
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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59 SERESIEVGIDVINAYVVAYRAGSQSYFL---RDAPASASTYLFPGTQ-RYSLRFDGSYG 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 DLERWAHOTREEISLGLQALTHAIS---FLRSGASNDEEKARTLIVIIOMASEAARYRCI 171
                         142 DNLETAAGTRRESIELGPNPLDGAITSLWY--DGG-----VARSLLVLIQMVPEAARFRY 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93132798; PubMed=8421313;
MEDLINE=93132798; PubMed=8421313;
Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;
Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;
Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;
Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;

Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;

J. Mol. Biol. 229:263-267(1993).

-!- CATALYTIC ANDIOTY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.

-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

EMBL; M98346; AAA32626.1;

--- FILED. TIARR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ODOVIKETTEGATSQSYKOFIEALROKLIGG--LIHDIPVLPDPTTVEERNYITVELSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 HABLSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD
                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Abrin-d (EC 3.2.2.2.2) (rRMA N-glycosidase) (Fragment).
Abrus precatorius (Indian licorice) (Crab's eye).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Rosidae;
eurosida I; Fabales; Rabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN
 124 DRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amatch 33.8%; Score 344.5; DB 10; Length 528; Local Similarity 45.0%; Pred. No. 5.9e-24; les 85; Conservative 24; Mismatches 71; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58870 MW; 62ED42FB8FFE60F8 CRC64;
                                                                                                                                                                                                          528 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; I. RIP; I.
SMART; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50231; RICIN B LECTIN; 2. PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q94KE4;
01-DEC-2001 (TrEMBLrel. 19, Created)
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                                                                                                                                                                                                            PRELIMINARY;
                                                                           184 IEGEMRTRIR 193
                                                                                                               195 İEQEVRRSLQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 EGEMRTRIR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 SNRVGVSIR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             528 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Toxin
                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                            206076
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ID 09
AC 09
DT 01
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                                   셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123
                                                                                                                                                                          183
                                                                                                                                                                                                                                                      142 DNIETRAGTRRESIELGPSPLDGAITSLYYDE----SVARSLLVVIOWVSEAARFRY 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 YPIINFTTAGAIVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 YPSVSFNLAGAKSTTYRDFLKNLRDRVATGTYEVNGLPVLRRESEVQVKNRFVLVRLTNY 87
                                                                             6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65
                                                                                                                 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Girbes T., Iglesias R., Perez Y., Ferreras J.M., Citores L.;
"Molecular cloning of ebulin 1.";
"Molecular cloning of ebulin 1.";
Submitted (ARF-2000) to the EMBL/GenBank/DDBJ databases.
-! CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 288 RRNA.
-! SIMILARITY: BELONGS TO THE RIBOSOWE-INACTIVATING PROTEIN FAMILY.
EMBL; AJ400822; CAC33178-1; -.
INTERPO: IPRO00772; Ricin_B_lectin.
InterPro; IPRO00772; Ricin_B_lectin.
FinterPro; IPRO1574; RIP.
Ffam; PF00652; Ricin_B_lectin; 6.
                                                                                                   28 YPSVSFNLAGAKSATYRDFLKNLRTIVATGTYEVNGLPVLRRESEVQVKNRFVLVLLTNY
                                                                                                                                                      66 AELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAI -- THLFTDVQNRYTFAFGGNY
                                                                                                                                                                                                                              DRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Gaps
                                         15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, campanulids, Dipsacales, Adoxaceae, Sambucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 564;
   DB 10; Length 563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Ribosome-inactivating protein precursor (EC 3.2.2.22) (rRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8261681A6DB55CB8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34.1%; Score 347.5; DB 10;
41.1%; Pred. No. 3.4e-24;
tive 41; Mismatches 56;
                                     :95
   34.4%; Score 350.5; DB 1041.6%; Pred. No. 1.8e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EBULIN L A-CHAIN.
EBULIN L B-CHAIN.
                                         40; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS00271; RICIN B LECTIN; 2.
PROSITE; PS00275; SHIGA-RICIN; 1.
Glycosidase; Hydrolase; Signal; Toxin.
SIGNAL
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Best Local Similarity 41.1%
Matches 78; Conservative
                                         79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                             195 IEQEVRRSLQ 204
                                                                                                                                                                                                                                                                                                         184 IEGEMRTRIR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               564
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sambucus ebulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-glycosidase).
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                                         Matches
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Pfam, PF00161; RIP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 SVTLALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 TISVAIDVTINVYIMGYRAGDISYFF---NEASATEAAKYVFKDSMRKITLPYSGNYERLQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 TAAGKIRENIPLGLPALDSAITTLFYYNAN----SAASALMVLIOSTSEAARYKFIEQQ 193
                                                                                                                                                                                                                                                                                                                                                                                                                                    9 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phan Van Chi, Nguyen Thuy Ha, Le Tran Binh;
"Genomic DNA Clone for mature typ-1 ribosome-inactivating protein from
"Trichosanthes sp. sample 01 Bac Kan 8-98 Vien CNSH (Hanoi).";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-! CATALYTIC ACTIVITY: EMBL/GenBank/DDBJ databases.
SPECIFIC ADENOSINE ON THE 28S RRNA.
-! SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
-! BMBL, AB039324; BAA92530.1; -
                                                                                                                                                        Yuan H., Wang L., Wang Y., An C., Chen Z.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I; Cucurbitales, Cucurbitaceae, Trichosanthes.
                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                                                                                                                                                                                                                                                                                                          12; Gaps
                                                                                                                                                                                         SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL, AF367252, AAK52960.1, -.
InterPro, IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                             Length 289;
          01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Trichosanthin precursor (EC 3.2.2.22) (rRNA N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Trichobakin (EC 3.2.2.2) (rRNA N-glycosidase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                          54; Indels
                                                                                                                                                                                                                                                                                                                                 24 270 TRICHOSANTHIN.
289 AA; 31706 MW; A6D5602549CA5657 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                           33.4%; Score 340; DB 10;
39.5%; Pred. No. 6.8e-24;
tive 46; Mismatches 54.
                                                      Trichosanthes kirilowii (Mongolian snake-gourd)
                                                                                                                                                                                                                                                                                                                      POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                        PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bac Kan 8-98.
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Eukaryota, Viridiplantae,
                                                                                                                                                                                                                                        Pro; IPR001574; RIP.
PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                     Hydrolase; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                        73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP, P09989; 1MRJ.
InterPro; 1PR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MRTRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 IGKRV 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                               NCBI_TaxID=3677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000
01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9LRE3;
                                                                                                                                                                                                                                                                                                                      SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 IISVAIDVINVYVMGYRAGDISYFF---NEASATEAAKKYVFKDAKRKVTLPYSGNYERLQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 IISVAIDVTSVYIMGYRAGDISYFF---NEASATEAAKYVFKDAMRKVTLPYSGNYERLQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 SVTLALDVINAXVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 127
                                                                                                                                                                                                                                                                                                                                       68
                                                                                                                                                                                                                                                                                                                                                                          2 VSFRLSGATSSSYGVFISNLRKALPYERKL-YDIPLL--RSTLPGSQRYALIHLTNYADE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 INFITAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94271613; PubMed=8003348;
Zeheng H., Wang B., Shaw P., Yeung H.;
Zchoning and DNA sequencing of the gene encoding trichosanthin].";
I Chuan Heuch Pao 21:42-51(1994).
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RENA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                       9 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I, Cucurbitales, Cucurbitaceae, Trichosanthes.
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Best Local Similarity 39.5%; Pred. No. 1.1e-23;
Matches 73; Conservative 46; Mismatches 54; Indels 12; Gaps
                                                                                                                                                                                                                                                                              12; Gaps
                                                                                                                                                                                                                     Length 247;
                                                                                                                                                                                                                                                                           53; Indels
                                                                                         1 1
247 247
247 AA; 27199 MW; 89811AC32892F03F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Trichosanthin (EC 3.2.2.22) (TRNA N-glycosidase).
TRICHOSANTHIN, T.CS.
                                                                                                                                                                                                              Query Match
33.2%; Score 338; DB 10;
Best Local Similarity 40.0%; Pred. No. 8.5e-24;
Matches 74; Conservative 46; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trichosanthes kirilowii (Mongolian snake-gourd)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
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PROSITE; PS00275; SHIGA_RICIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001574; RIP. Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 IGKRV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 MRTRI 192
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                                                            Hydrolase; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Toxin.
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                                                                                            NON TER
NON TER
SEQUENCE
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IISSUE=Leaf
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                                                                                       RESULT 13
Q945S2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 SVTLALDVTNAXVVGYRAGNSAYFFHPDNQEDAEALTHLFTDVQNRYTFAFGGNYDRLEQ 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 LAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 188
                           9
128 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ONE
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                                                                                                                                                                                                                                                                                                                                                                                                                 Abrus precatorius (Indian licorice) (Crab's eye).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, Core eudicots, Rosidae,
eurosids I, Fabales, Fabaceae, Papilionoideae, Abreae, Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT C SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SUBGINIT DISULEDE-LINKED DIMER OF A AND B CHAINS.
-!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOMOLOGOUS SUBDOWALINS (ALPHA, BETA, GAMMA).
-!- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING PROTEINS. BELONGS TO TYPE 2 RIP.
-- SIMILARITY: TO ANABOSOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Evensen G., Mathiesen A., Sundan A.; "Direct molecular cloning and expression of two distinct abrin A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABRIN-A IS MORE TOXIC THAN RICIN.
FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; renovation of Prints of Prints of Providers of Providers of Providers of Prints of Providers of Pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 AA; 28309 MW; BBFC846B9E92B5DE CRC64;
                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Abrin-E (RRNA N-glycosidase) (EC 3.2.2.22) (Fragment)
                                                                                                                                                                                                                                                                                                                                   Last sequence update)
                                                                                                                                                                                                                                                             252 AA.
                                                                                                                                                                                                                                                                                                          01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 266:6848-6852(1991).
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hes 83; Conservative
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                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                            188 MRTRI 192
                                                                                                                                          194 IGKRV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=LEAF
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                                                                                                                                                                                                                                                                                    038760;
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                                                                                                                                                                                                                RESULT 12
                                                                                                                                                                                                                                      038760
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124 DRLEQLAGNLRENIELGNGPLEBAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQY 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 YPSVSFNLDGAKSATYRDFLSNLRKTVATGTYEVNGLPVLRRESEVQVKSRFVLVPLTNY 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteins from Sambucus nigra leaves.";
Submitted (AUG-2001) to the RMBL/GenBank/DDBJ databases.
-- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RRAN.
-- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
BMBL, FA409133.1; --
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PR001594; RIP.
PRINTS; RR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 YPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILVELSNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 NGNTVTLAVDVTNLYVVAFSGNANSYFF-----KDATEVQKSNLFVGTKQN-TLSFTGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                          Sambucus nigra (European elder).

Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
Asteridae, campanulids; Dipsacales; Adoxaceae; Sambucus.

NCBI_TaxID=4202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sambucus nigra (European elder).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Characterization and cloning of lectins and ribosome-inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 330.5; DB 10; Length ; Pred. No. 1.4e-22; 39; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Type 2 ribosome-inactivating protein nigrin 1 precursor (EC 3.2.2.22).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62242 MW; 07F7CBEDCF33BF10 CRC64;
                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Ribosome-inactivating protein (EC 3.2.2.22) (TRNA N-glycosidase)
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                                                                                                                                                      563 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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Best Local Similarity 39...
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SEQUENCE 563 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
177 GVSİR 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 DNLETAANTRRESIELGPSPLDGAITSLYHGD-----SVARSLLVVIQMVSEAARFRY 194
                                                                                                                                                                                                                                                                                                                                           6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65
                                                                                                                                                                                                                                                                                                                                                                   29 YPSVSFNLDGAKSATYRDFLSNLRKTVATGTYEVNGLPVIRRESEVQVKSRFVLVPLTNY 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94139756; PubMed=8307038; Chih.Hung H., Lee M.C., Chen J.K., Lin J.Y.; Chih.Hung H., Lee M.C., Chen J.K., Lin J.Y.; Clohing and expression of three abrin A-chains and their mutants derived by site-specific mutagenesis in Escherichia coli."; Eur. J. Blochem. 219:83-87 (1994).
                                                                                                              Girbes T., Arias F.J., Antolin P.; "Characterization and molecular cloning of Nigrin 1, a type two ribosome-inactivating protein from leaves of elder (Sambucus nigra)."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Abrus precatorius (Indian licorice) (Crab's eye).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.

NCBL_TaxID=3816;
                                                                                                                                                                                                                                                                                                            15; Gaps
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EMBL; X54873; CAA38655.1; -.
EMBL; X76720; CAA54138.1; -.
HSSP; P11140; 1ABR.
InterPro; IPRO01274; RIP.
PF00161; RIP; 1.
                                                                                                                                                                                                                                                                32.4%; Score 330.5; DB 10; Length 563; 39.5%; Pred. No. 1.4e-22; tive 39; Mismatches 61; Indels 15;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
NCBI_TaxID=4202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Evensen G., Mathiesen A., Sundan A.;
Submitted (OCT-1990) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 22, Last annocation update)
01-OCT-2002 (TrEMBLrel. 22, Last annocation update)
Ricin A-chain type 73 (EC 3.2.2.22) (FRNA N-glycosidase)
                                                                                                                                                                                     EMBL, AF249280; AAN66130.1; -.
Hydrolase; Glycosidase.
SEQUENCE 563 AA; 62173 MW; 0RB236421FC5E04F CRC64;
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PROSITE; PS00275; SHIGA_RICIN; 1.
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Best Local Similarity 39.5#
Matches 75; Conservative
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|EQEVRRSLQ 204
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                                                                                                                           9 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 68
                                                                                                                                                                                           69 SVTLALDVTNAYVVGYRAGNSAYFFH--PDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL
                                                                                            13; Gaps
                                                           32.3%; Score 329.5; DB 10; Length 252;
42.8%; Pred. No. 5.5e-23;
                                                                                            66; Indels
             252 252 252 2823 MW; 187B8B4E134AECE5 CRC64;
                                                                                           Conservative 28; Mismatches
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ne : 27.4196 secs
Glycosidase; Hydrolase; Toxin.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result.being printed, and is derived by analysis of the total score distribution.

			Description	Ricin A from pICI1	Amino acid sequenc	Ricin A chain. Un	Ricin A-chain (RTA	Ricin A-chain ribo	Ricin A-chain RIP.	Ricin A. Escheric	Sequence of Ricinu	Ricin A encoded by
SUMMAKIES			a a	AAR30722	AAB19265	AAR37290	16 AAR63902	AAW25136	AAW21699	AAP70097	AAP70838	AAP95639
			DB	13	21	14	16	18	18	80	00	10
			re Match Length DB I	267	267	267	267	290	290	332	332	332
	æ	Query	Match	98.4	98.4	97.5	97.5	97.5	97.5	97.5	97.5	97.5
			Score	950	950	941	941	941	941	941	941	941
		Result	No.	1	2	ď	4	Ŋ	9	7	00	σ

Anti-cataract immu Ricin D. Ricinus	ο£	Castor bean prepro	Modified castor be		Castorbean ricin.		Ricinus communis r	Castor bean prepro	r i	Biosynthetic multi		0	Sequence of Ricinu	G	Sequence of G-FIT.	g	Ricin A. Syntheti	Ricin A chain (RTA	Castor oil plant a	R. communis agglut	Sequence of Ricin	Ricin agglutinin A	Trichosanthin anti	Amino acid sequenc	Synthetic alpha-tr	Mature alpha-Trich	Trichosanthin (a r			Trichosanthin from	Trichosanthin prot	Encodes chinese cu	Alpha-trichosanthi	Chinese cucumber a
AAR70827 AAP90079	AAP50166	AAG78300		4	AAW25787					AAP80164	AAP60240	AAR39570	AAP70325				AAR32430			AAW21706	AAP70324						1 AAW25140		. AAR07514				. AAR55129	AAW10468
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ALIGNMENTS

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pH; temperature; cultivation; host; soluble.
     AAR30722 standard; Protein; 267 AA
                                                                                                                                                                                                           Kara BV;
                                                                                                                                                                                   (ICIL ) IMPERIAL CHEM IND PLC. (ZENE ) ZENECA LTD.
                                                                                                                                                     91GB-0003925.
91GB-0003926.
91GB-0004016.
                                                                                                                                      92EP-0301466
                                   (updated)
(first entry)
                                                                                                                                                                                                           Fitton JE, Hockney RC,
                                                          Ricin A from pICI1102.
                                                                                                                                                                                                                         WPI; 1992-294124/36.
N-PSDB; AAQ27876.
                                                                                                                                                     26-FEB-1991;
26-FEB-1991;
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08-FEB-1993
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Sequence
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                                                                                                                                                                                                                                                                                                                                               110
                                                                                                                                                                                                                                                                                                                                                                     61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
                                                                                                                                                                                                                                                                                                                                                                                             GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 170
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                                                                                                                                                                                                                                                                                                                                               ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEA1THLFTDVQNRYTFAFG
                                                                            Prepn. of ricin A comprises cultivating a host, including a DNA sequence which encodes ricin A, e.g. from pICII102, in a nutrient medium for an initial period at a first pH value which favours growth of the host; and cultivation the host for a further period at a pH lower than the first pH value, and opt. cooling the host during the terminal portion of the cultivation and harvesting the host during the the terminal portion. By adjusting the pH and temp. during the cultivation of hosts, high yields of soluble recombinant ricin A
                                                                                                                                                                                                                                                                          10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "vascular leak syndrome (VLS) inducing motif"
           Prepn. of soluble recombinant polypeptide(s), esp. ricin A - by adjusting pH and/or temp. during cultivation to increase yield of
                                                                                                                                                                                                                                                 98.4%; Score 950; DB 13; Length 267; 94.9%; Pred. No. 1.1e-93; ive 0; Mismatches 0; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of a human ricin toxin A chain (RTA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ghetie VF, Baluna RG, Smallshaw J;
                                                                                                                                                                                        (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB19265 standard; protein; 267 AA
                                                         Disclosure; Fig 9; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                           171 FOYIEGEMRTRIRYNRRS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FOYIEGEMRTRIRYNRRS 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TEXA ) UNIV TEXAS SYSTEM
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Matches 188; Conservative
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                                                                                                                                                                              are obtained.
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                                                                                                                                                                                                                             Sequence
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121 GNYDRLEOLAGNIRENIELGNGPLEEAISALYYYSTGGTOLPTLARSFIICIOMISEAAR 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
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                                                 Modifying the ability of a proteinaceous composition to induce a toxic effect for reducing vascular leak syndrome, comprises identifying at least one specified amino acid sequence and altering it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                            The specification describes a method for producing immunotoxins and cytokines with a reduced ability to promote vascular leak syndrome (VLS). The immunotoxins are useful for treating graft versus host disease, non-Hodgkin's and Hodgkin's lymphoma, myeloma, metastatic lesion tumours and some type of solid tumours. The present sequence represents an immunotoxin (ricin toxin A chain) which induces VLS. The VLS-inducing motif can be mutated or deleted so that VLS is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Type II ribosome-inactivating protein; type II RIP; gelonin; momordin; immunoconjugate; autoimmune disease; cell killing; toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 267;
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Pred. No. 1.1e-93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MVPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
                                                                                                                                                                Example 1; Page 119-120; 125pp; English.
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WPI; 2000-664922/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 AA;
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SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 112
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                                                                                                                                                                                                 The invention covers analogues of Type I RIPs. Ricin is a Type II RIP whose A chain is homologous to plant type I RIPs. The analogues of the invention have a cysteine available for intermolecular disulphide bonding at an amino acid position corresp. to a position not naturally available for bonding; the cys residue is located in the C-terminal region of the analogue between a position corresp. to amino acid 251 and the C-terminus of ricin A chain. The analogues are pref. joined via a disulphide linkage to a molecule which specifically binds to a target cell, e.g. an antibody fragment. (Updated on 09-JAM-2003 to acorrect PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----VLPNRVGLPINQRFILVEL
Analogues of type I ribosome inactivating protein - useful as cytotoxic agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in-vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                         Claim 1; Page 92; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 YIEGEMRTRIRYNRRS 188
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27-JUL-1995
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 YDRLEQLAGNIRENIELGNGPLEEAISALYYSTGGTQLPTLARSFIICTQMISEAARFQ 182
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                                                                                                                                                                                                                                                                                                                                                                                                             3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILVEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maize; proRIP; ribosome inactivating protein; alpha; beta subunit; internal linker; Barley Tranalation Inhibitor; Trichosanthin; Ricin A-chain; Abrih-A A-chain; Aporin; SIT-1; Luffin A; MAP; Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30; therapeutic toxin; tumour cell targeted; protein synthesis inhibitor; post-translational modification; cancer; neoplasia; HIV: AIDS; human immunodeficiency virus; acquired immune deficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                           10; Gaps
                                                                              AAR63902 is the ricin A chain gene product, it is analogous to the ribosome-inactivating proteins (RIPs) described in AAR63903-R63911 RIPs are the key components of cytotoxic therapeutic agents (CTAs), which include gene fusion products and immunoconjugates. CTAs may be used to selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host
                                                                                                                                                                                                                                                                                                                                      Score 941; DB 16; Length 267;
Pred. No. 1e-92;
0; Mismatches 0; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ricin A-chain ribosome inhibitory protein inactive precursor.
which are suitable for use as components of cytotoxic
                                                                                                                                                                                                                                                               (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW25136 standard; Protein; 290 AA.
                                                Example 3; Fig 1; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 YIEGEMRTRIRYNRRS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 YIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92US-0987927.
90US-0535636.
95US-0378761.
                                                                                                                                                                                                                                                                                                                                      97.5%;
94.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-0485286.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                        Matches 186; Conservative
                therapeutic agents.
                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                      267 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
02-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US5646026-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-JAN-1995,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW25136;
                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113
                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                   disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW25136
셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
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(DOWC) DOWELANCO.

ij

inactive be expressed in

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AAW25136 represents a Ricin A-chain ribosome inhibitory protein (RIP)
which was engineered to contain a selectively removable internal peptide
linker sequence separating the alpha and beta units of the RIP. When
separated the two units regain activity and are capable of inactivating
eukaryotic ribosomes and hence preventing protein production. Many
different RIPS may be produced with an internal linker including
maize RIP, Trichosanthin, Ricin A-chain, Abrin-A A-chain and
Saporin. The RIPs can be used in the construction of therapeutic
toxins targeted to specific cells such as the
tatachment of a targeting polypeptide, e.g. a monoclonal antibody.
A further use is in HIV therapy (see US4869903). There is interest
the capacity to provide correct post-translational processing However,
RIPs effectively inhibit protein synthesis in eukaryotic cells, hewever,
in capacity to provide correct post-translational processing. However,
RIPs effectively inhibit protein synthesis in eukaryotic cells resulting
in cell death. Since the inactive RIP proteins are not cytotoxic to
cukaryotic cells, they can be recombinantly expressed in such cells and
then converted to active RIP proteins.
(Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 PKQYPIINFTTAGAIVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inactivation; eukaryotic ribosome; alpha fragment; beta fragment; inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver; rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.5%; Score 941; DB 18; Length 290; 94.9%; Pred. No. 1.1e-92; Live 0; Mismatches 0; Indels 10
                                                                                                  DNA encoding pro-ribosome inactivating proteins -
precursors of ribosome inactivating proteins; can
eukaryotic cells without causing cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT---
                                                                                                                                                                                    Claim 4; Column 91-94; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
152..162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW21699 standard; Protein; 290 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 YIEGEMRTRIRYNRRS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YIEGEMRTRIRYNRRS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                             WPI; 1997-362934/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ricin A-chain RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
26-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW21699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW21699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
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112

96

-----VLPNRVGLPINQRFILVEL

10; Gaps

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The sequences given in AAW21698-710 represent Ribosome Inactivating Proteins (RIP's), which may be used in the construction of the proteins (RIP's), which may be used in the construction of the protein be the invention. The proRIP has a selectively removable, internal peptide linker. The procursor sequence is incapable of inactivating eukaryotic ribosomes, but can be converted by removal of the linker into a protein having alpha and beta fragments and being capable of inactivating eukaryotic ribosomes. RIPs are potent inhibitors of eukaryotic protein synthesis. They possess a highly specific N-glycosidase activity which cleaves the glycosidic bond of adeniar proliferation of cells, e.g. cancer cells and HIV-infected T cellular proliferation of cells, e.g. cancer cells and HIV-infected T cells. The inactive proRIP proteins make it possible to provide protein possible. The RIP can be used to make cytotoxic conjugates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 SNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----VLPNRVGLPINORFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 PKÓYPIINFTTAGATVÓSÝTNFIRAVRGRLÍTTGADVRHEIPVLÞNRVGLÞINQRFILVEL
/note= "Position of possible insertion of internal
                                                                                                                                                                                                                                                                                                                                             Inactive precursor of maize ribosome-inactivating protein - also
chimeric ribosome-inactivating protein precursors containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.5%; Score 941; DB 18; Length 29(94.9%; Pred. No. 1.1e-92; ... Mismatches 0; Indels
                   peptide linker sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT---
                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Column 91-94; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP70097 standard; protein; 332 AA.
                                                                                                                                                                                                                                                                       Walsh TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173 YIEGEMRTRIRYNRRS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 YIEGEMRTRIRYNRRS 222
                                                                                                                         95US-0378761
                                                                                                                                                                               90US-0535636.
                                                                                                                                                              92US-0987927
                                                                                                                                                                                                95US-0378761
                                                                                                                                                                                                                                                                                                                                                                                   internal linker sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 186; Conservative
                                                                                                                                                                                                                                                                       Morgan AER,
                                                                                                                                                                                                                                                                                                           WPI; 1997-309831/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                    DOWC ) DOWELANCO.
                                                                                                                         26-JAN-1995;
                                                                                                                                                              09-DEC-1992;
                                                                                                                                                                               11-JUN-1990;
26-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-APR-1991
                                                     US5635384-A
                                                                                         03 - JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP70097;
                                                                                                                                                                                                                                                                        Hey TD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ricin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP70097
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146

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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICTQMISEAARFQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----VLPNRVGLPINQRFILVEL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence of Ricinus communis castor beans ricin toxin (RT or ricin) A protein encoded by pRA123.
                                                                                                                                                                                                                                                                                                                                                                                                                           N-terminal methionine free proteins prodn. - by using host transformed with vector to express a methionine-amino-peptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ricin A may be produced in a form which lacks an N-terminal Metusing Met-aminopeptidase from E.coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.5%; Score 941; DB 8; Length 332; 94.9%; Pred. No. 1.4e-92; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lectin; toxin protein; cytotoxic; cytostatic; castor bean;
                                                                                                                                                                                                                                                                                                                             Chang SY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP70838 standard; protein; 332 AA.
                                                                                                                                                                                                                                                                                                                             Chang S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Fig. 4; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l..32
'note="Leader"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 YIEGEMRTRIRYNRRS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 YIEGEMRTRIRYNRRS 233
                                                                                                                                                                               86EP-0307242.
                                                                                                                                                                                                                        86US-0860330
                 Ricin A; Met-aminopeptidase.
                                                                                                                                                                                                                                           85US-0778414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                           Benbassat A, Bauer KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33..302
                                                                                                                                                                                                                                                                                                                                                                    WPI; 1987-110172/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                  (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAN70152
                                                       Escherichia coli
                                                                                                                                                                               19-SEP-1986;
                                                                                                                                                                                                                        06-MAY-1986;
                                                                                                                                                                                                                                              20-SEP-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
18-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plant toxin.
                                                                                                                                         22-APR-1987
                                                                                                EP219237-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP70838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP70838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE ELECTRIC SERVICE STATES AND SERVICE SERVICES AND SERV
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The full-length sequences encoding ricin A (AAN70520), ricin D (AAN70525), putative ricin E (AAN70526) and RCA (AAN70524) in precursor form were obtch. using messenger RNA to obtain a cDNA library, and then probing the library to retrieve the desired cDNA library. The library was probed using the 35-mer given in AAN70514. Figure 4 (see AAN70520, AAN70522) shows the nucleotide sequences of three plasmids contg. cDNA inserts obtd. by probing a cDNA library for sequences encoding ricin B using the probing a CDNA library for sequences encoding ricin B using the probing a CDNA library for sequences may be used to place an ATG start codon and a Hindlil site at the beginning of the mature protein (see AAN70518). The coding sequences of the inserts can be ligated into expression vectors contg. the PhoA promoter-operator and leader sequence (AAN70523) and suitable retroregulators.

(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 YDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 SNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYIFAFGGN 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.5%; Score 941; DB 8; Length 332;
94.9%; Pred. No. 1.4e-92;
tive 0; Mismatches 0; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New non-glycosylated ricin precursor and toxin etc. - are prepd. by recombinant DNA procedures with specific isolation steps for purer and soluble prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP95639 standard; protein; 332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1; 112pp; English.
/note="A-chain"
315..332
                                  315..332
/note="B-chain"
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                                                                                                                                                                                                                                                                         86EP-0308877
                                                                                                                                                                                                                                                                                                                                           86US-0837583
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Best Local Similarity 94.9%
Matches 186; Conservative
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(updated)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      (CETU ) CETUS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAN70519
                                                                                                                                                                                                                                                                         13-NOV-1986;
                                                                                                                                                                                                                                                                                                                                           07-MAR-1986;
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31-OCT-2002
                                                                                                                                                                                                      23-SEP-1987
                                                                                                                                    EP237676-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Piatak M;
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173 YIEGEMRTRIRYNRRS 188
           218 YIEGEMRTRIRYNRRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                   WO9503828-A1
                                                                                                        25-MAR-2003
31-AUG-1995
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                                                                                                                                                                                                 Synthetic.
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                                                                                     AAR70827;
                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                           Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 172
                                                                                                                                                                                                                                                                                                                                                                                       Recombinant vectors expressing ricin chains or diphtheria toxin -used for prodn. of new immunotoxin conjugates with monoclonal antibodies, having high cell specificity and good extracellular stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 YDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILVEL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 PKÓYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILVEL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid RA123 (ATCC No. 39799) carries the entire coding sequence for ricin A, as well as codons for 12 AAs joining the A to the B chain. Following modification for ease of manipulation the plasmid was used to construct expression vectors which express the conjugates in
                                                                                                                                                                                                                                                                                                                               Kaplan D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.5%; Score 941; DB 10; Length 332; 94.9%; Pred. No. 1.4e-92; ive 0; Mismatches 0; Indels 10
                                                                                                                                                                                                                                                                                                                              Lawyer FC, Horn G, Greenfield L, Nitecki D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           host cells. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.)
                                     Plasmid pRA123; ricin-A; ricin-B; cytotoxicity
                   Ricin A encoded by insert from plasmid pRA123
                                                                                                 1..35
'label= leader sequence
                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 14; 54pp; English.
                                                                                                                                       303..314
/label=linker
315..332
/label=B-chain
                                                                                                                            /label=A-chain
                                                                                                                                                                                                                                                84US-0578115.
84US-0578121.
84US-0578122.
84US-0648759.
84US-0653515.
                                                                                                                                                                                                                              89EP-0201162
                                                                                                                                                                                                                                                                                                           (CETU ) CETUS CORPORATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 94.9
les 186; Conservative
                                                                                                                                                                                                                                                                                                                                                            WPI; 1989-286959/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     332 AA;
                                                         Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAN91281
                                                                                                                                                                                                                              19-JAN-1989;
                                                                                                                                                                                                                                                                             07-SEP-1984;
20-SEP-1984;
                                                                                                                                                                                                                                                                      09-FEB-1984;
                                                                                                                                                                                                                                                 08-FEB-1984;
                                                                                                                                                                                                                                                          08-FEB-1984;
13-AUG-1990
                                                                                                                                                                                                           04-OCT-1989
                                                                                                                                                                                                                                                                                                                              Gelfand D,
                                                                                                                                                                                        EP335476-A.
                                                                                                                                                                                                                                                                                                                                          Piatak MJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113
                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                Peptide
                                                                                                                   Peptide
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The immunotoxin given in AAR70827 comprises the heavy and light chain variable regions of anti-lens epithelium IgG3 MAb 4197X linked to ricin-A and a hexa-histidine tag. The DNA construct encoding the immunotoxin was expressed from pHB19 in E. coli. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                              Immunotoxin; heavy chain; light chain; variable region; antibody; ricin-A; cytostatic; cataract; lens opacification; epithelial cell; pHB19; 4197X; monoclonal antibody; MAb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New single chain immuno:toxin - binds specifically to epithelial cells, for inhibiting development of sec. cataracts after extra:capsular cataract extraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 97.5%; Score 941; DB 16; Length 554; Best Local Similarity 94.9%; Pred. No. 2.7e-92; Matches 186; Conservative 0; Mismatches 0; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..27
|Tabel= Sig_peptide
|note= "phoA signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "MAb 4197X heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169..274
/label= LIGHT
/note= "MAb 419X light chain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "hexa-histidine tail"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gould RM, Kelleher PJ, Wallace TL,
                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
AAR70827 standard; Protein; 554 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig.4; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          276..544
/label= RICIN-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label= LINKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28..145
/label= HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94WO-US07919.
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                                                                                                              (updated)
(first entry)
                                                                                                                                                                                               Anti-cataract immunotoxin.
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                  280 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 339
                                                           112
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                                                                                                                                                 459
                                                                                                                                    400 YDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ
                                                           SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN
                                                                                                                    113 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ
 -----VLPNRVGLPINQRFILVEL
                                                                                     340 SNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYTFAFGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ricin D (see corresp. AAN90068) found on the EcoRI-HindIII fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of DNA from Ricinu communis, Zanibariensis variety. Patent discloses many modifications of ricin in which the lectin binding function of the B chain is diminished or removed, and conjugation to toxins to eliminate cell binding. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                        Ricin D; Ricinus communis; caster beans; Zanibariensis variety; modified; lectin binding removed; reduced cell binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97.5%; Score 941; DB 10; Length 562; 94.9%; Pred. No. 2.8e-92; ive 0; Mismatches 0; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified ricin molecules and toxin conjugates - in which the lectin binding function of the B chain is removed or diminished to reduce cell binding.
PKQYPIINFTTAGATVQSYTNFIRAVRGRLT--
                                                                                                                                                                                                                                                                                     AAP90079 standard; protein; 562 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; fig 1; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ricinus communis (caster beans)
                                                                                                                                                                               173 YIEGEMRTRIRYNRRS 188
                                                                                                                                                                                                           460 YIEGEMRTRIRYNRRS 475
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 94.9:
Matches 186; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          562 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAN90068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-NOV-1987;
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                                                                                                                                                                                                                                                                                                                                                              01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brown EL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                           53
                                                                                                                                                                                                                                                                                                                 AAP90079;
                                                                                                                                                                                                                                                                                                                                                                                            Ricin D.
                                                                                                                                                                                                                                                       RESULT 11
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53 SNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 112

38 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 97

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3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILVEL

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98 SNHABELSVILALDVTNAYVVGYRAGNSAYFFHPDNQEDABAITHLFTDVQNRYTFAFGGN 157
                                                      113 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preproricin is the whole polypeptide encoded by AAN50202 and the DNA encoding this is claimed. Proricin is obtained from preproricin by removal of the AA leader sequence. The linker AA sequence which is present in the precursor polypeptide is enzymatically removed in the cell to separate the A and B chains, which are joined by a disulphide bridge during the formation of the ricin molecule itself. This linker region as well as the presumptive amino terminal leader or signal sequence are not present in the sequences already published by Funatsu et al.
                                                                                                                                                                                                                                                                                                                                                                           25..365
292..303
/label= links the C-terminus of the A chain and
the N-terminus of the B chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New DNA sequences coding for ricin type plant toxin - or its mutants, and modified vectors and host microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                           260..262
/label= N-linked glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   398.400
/label= N-linked glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               438..440
/label= N-linked glycosylation
                                                                                                                                                                                                                                                              Sequence of preproricin encoded by pRCL617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure, Page 30-30c; 40pp; English.
                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                   AAP50166 standard; Protein; 565 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lamb FI;
                                                                                                                                                                                                                                                                                                                                                                     'label= signal
                                                                                           173 YIEGEMRTRIRYNRRS 188
                                                                                                                  218 YIEGEMRTRIRYNRRS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84GB-0006569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83GB-0019265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84EP-0304801.
                                                                                                                                                                                                                                                                                        Toxin, anti-tumour therapy
                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lord JM, Roberts LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYWA-) UNIV WARWICK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1985-148040/25.
N-PSDB; AAN50202.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAR-1984;
15-JUL-1983;
15-JUL-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JUL-1984;
                                                                                                                                                                                                                                     16-0CT-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP145111-A.
                                                                                                                                                                                                                                                                                                                  Ricinus.
                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                         RESULT 12
AAP50166
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Cleavage-site
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                                                                                                 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 112
                                                                                                                                    113 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 172
                                                                                                                                               147 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 206
                                                             52
                                                                              86
                                                                                                                                                                                                                                                                                                                                                                                                                                                    303..565
/label= Ricin_B_chain
/note= "Galactose/N-acetylgalactosamine-binding lectin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel composition comprising toxin e.g., ricin based antiviral compound useful for treating viral infections such as human immunodeficiency
                                                                                                              SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN
                                                                             PKOYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHDIPVLPNRVGLPINQRFILVEL
                                                             ----VLPNRVGLPINORFILVEL
                                                                                                                                                                                                                                                                                                              Castor bean plant, preproricin; ricin; A chain; B chain; human immunodeficiency virus infection; HIV; toxin; antiviral agent; retroviral infection; anti-HIV; virucide activity; viral protease.
                                            Gaps
                                          0; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                          291..302
/label= Linker_peptide
/note= "Cleaved during activation of ricin"
                        97.5%; Score 941; DB 6; Length 565; 94.9%; Pred. No. 2.8e-92; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                             Castor bean preproricin protein (SEQ ID 1).
                                                             PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
                                                                                                                                                                                                                                                                                                                                                                                               25..290
/label= Ricin A chain
/note= "N-glycosidase"
                                                                                                                                                                                                                                                                                                                                                                              1..24
/label= Signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 47-50; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                       AAG78300 standard; Protein; 565 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BECH-) BECHTEL BWXT IDAHO LLC.
                                                                                                                                                                                   YIEGEMRIRIRYNRRS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-FEB-2000; 2000US-0182759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-FEB-2001; 2001WO-US05282
                                                                                                                                                                                                                                                                          15-NOV-2001 (first entry)
                                          Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-581908/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ward TE;
                         Query Match
Best Local Similarity
       565 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAI64137.
                                                                                                                                                                                                                                                                                                                                                    Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200160393-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Keener WK,
                                                             m
                                                                              27
                                                                                                 53
                                                                                                                  87
                                                                                                                                                                                          207
                                                                                                                                                                                                                                                        AAG78300;
                                                                                                                                                                        173
       Sequence
                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                               AAG78300
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The sequence relates to preproricin protein encoded by the DNA sequence given in AAI64137. The invention relates to a novel toxin (e.g., ricin) based antiviral agent which is toxic to virus-infected cells, but non-toxic to uninfected cells. The invention has anti-HIV and virucide activities. Its mechanism of action is through inactivation of cellular ribosomes and enhancement of binding of the antiviral agent to galactose residues on cell surfaces, and its cellular internalisation. The invention is useful for treating human immunodeficiency virus infection and other viral infections, especially retroviral infections. The invention is useful for treating human immunodeficiency virus infection and other viral infections, especially retroviral infections. The integration of the viral genome into the host genome thereby preventing the latency/rebound problem. The agent enters all HIV susceptible cells, and not just cells known to act as host cells for the virus. The autiviral agent remains inert in a cell until degraded in it, unless the autiviral agent the virus, where the viral protease activates it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>٦</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 YDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICTQMISEAARFQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 YDRIEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Proricin consists of the ricin A chain, a linker peptide, and the ricin B chain. Proricin is proteolytically cleaved between the A chain and the linker to yield mature ricin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -VLPNRVGLPINQRFILVEL 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 PKÓYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHDIPVLPNRVGLPINQRFILVEL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human immunodeficiency virus infection, HIV, toxin, antiviral agent, retroviral infection, anti-HIV, virucide, viral protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 941; DB 22; Length 56: Pred. No. 2.8e-92; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Castor bean plant; preproricin; ricin; A chain; B chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric - Ricinus communis
Chimeric - Human immunodeficiency virus type 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified castor bean preproricin (SEQ ID 10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Signal peptide
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/label= Linker_peptide
296..297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "N-glycosidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25..291
/label= Ricin_A_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG78304 standard; Protein; 565 AA.
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/label= Proricin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 YIEGEMRTRIRYNRRS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 YIEGEMRTRIRYNRRS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.5%;
94.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al Similarity 94.9
186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                565 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-NOV-2001
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Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence relates to the amino acid sequence of a modified preproricin protein encoded by AMI64145. The invention relates to a novel toxin (e.g. ricin) based antiviral agent which is toxic to virus-infected cells, but non-toxic to uninfected cells. The invention has anti-HIV and virucide activities. The agent is able to enter all HIV susceptible virucide activities. The agent is able to enter all HIV susceptible antiviral agent remains inert in a cell unless the cell is infected with the HIV virus, where the viral protease activates it. Ricin's mechanism of action is through inactivation of cellular ribosomes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFO 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 YDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enhancement of binding of the antiviral agent to galactose residues on cell surfaces, and its cellular internalisation. The invention is useful for treating human immunodeficiency virus infection and other viral infections, especially retroviral infections. The antiviral agent is activated in viral particles or early stage infected cells, killing the cells upon infection and effectively preventing the integration of the viral genome into the host genome thereby preventing the latency/rebound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 PKOYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 86
                                                                                                                                                                                                                                                                                                                                                                                                                     Novel composition comprising toxin e.g., ricin based antiviral compound useful for treating viral infections such as human immunodeficiency virus infection.
                                 /label="Ricin_B_chain
/note= "Galactose/N-acetylgalactosamine-binding lectin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 PKOYPIINFITAGATVOSYTNFIRAVRGRLT-------ULPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Gaps
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97.5%; Score 941; DB 22; Length 565;
Best Local Similarity 94.9%; Pred. No. 2.8e-92;
Matches 186; Conservative 0; Mismatches 0; Indels 10
/label= HIV_protease_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 59-63; 66pp; English.
                                                                                                                                                                                                                                                                       (BECH-) BECHTEL BWXT IDAHO LLC.
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                                                                                                                                                                                                                               16-FEB-2000; 2000US-0182759.
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                 304..565
/label= R
                                                                                                                                                                                                                                                                                                                 Keener WK, Ward TE;
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Best Local Similarity
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                 Protein
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AAP70326 standard; Protein; 576 AA.

RESULT 15

AAP70326;

AAP70326 ID AAP7 XX AC AAP7 XX

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The full length sequences encoding ricin A (AAN70520), ricin D

(AAN70525) putative ricin E (AAN70526) and RCA (AAN70524) in precursor

(Corm were obtained, using the messenger RNA to obtain a cDNA library,

then probing the library to retrieve the desired cDNA inserts. The

library was probed using the 35-mer given in AAN70514. Figure 4 (see

AAN70520, AAN70521, AAN70521, shows the nucleotide sequences of three

plasmids containing cDNA inserts obtained by probing a cDNA library

for sequences encoding ricin B using the probe in AAN70517. The CDNA

miserts can be placed into expression vectors. Site-directed

mutagenesis may be used to place an ATG start codon and a HindIII

site at the beginning of the mature protein, (see AAN70518). The

coding sequences of the inserts can be ligated into expression

vectors containing the PNOA promoter-operator and leader sequence

(AAN70523) and suitable retroregulators.

(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New non-glycosylated ricin precursor and toxin etc. - are prepd. by recombinant DNA procedures with specific isolation steps for purer and soluble prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97.5%; Score 941; DB 8; Length 576; 94.9%; Pred. No. 2.9e-92; live 0; Mismatches 0; Indels
                                                                                              Lectin; toxin protein; cytotoxic; cytostatic; castor bean;
                                             Sequence of Ricinus communis (castor bean) Ricin toxin (RT or ricin) E precursor encoded by pRT38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 14(1-2); 112pp; English.
                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                        315..576
/note= "B-chain"
                                                                                                                                                                                                                                       /note= "A-chain"
                                                                                                                                                                                                         'note= "leader"
                                                                                                                                                                                                                                                                                                                                                                       86EP-0308877
                                                                                                                                                                                                                                                                                                                                                                                                     86US-0837583
(updated)
(first entry)
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                                                                                                                                                                                                                            36..302
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                                                                                                                                                                                                                                                                                                                                                                                                                                   (CETU ) CETUS CORP. (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          576 AA;
                                                                                                                                             Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAN70526
                                                                                                                                                                                                                                                                                                                                                                     13-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                     07-MAR-1986;
                                                                                                                plant toxin.
                                                                                                                                                                                                                                                                                                                                       23-SEP-1987
             21-MAY-1991
                                                                                                                                                                                                                                                                                                       EP237676-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Piatak M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Region
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158 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 217 . අුධ දිර ව

qq

Search completed: February 10, 2004, 16:22:28 Job time : 33.0534 secs

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(without alignments)
930.966 Million cell updates/sec
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| SIDS1/gcgdata/geneseq/genesegp-emb1/AA1990.DAT:*
| SIDS1/gcgdata/geneseq/genesegp-emb1/AA191.DAT:*
| SIDS1/gcgdata/geneseq-genesegp-emb1/AA191.DAT:*
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2: \SIDSI\gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*

3: \SIDSI\gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*

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5: \SIDSI\gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1107863 segs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1025
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

7 N I N I N I N I N I N I N I N I N I N
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22 AAG78304 8 AAPT0026 18 AAW570326 18 AAXW57892 20 AAX58892 21 AAX78592 22 AAG78301 22 AAG78301 22 AAG78301 22 AAG78301 22 AAG78301 22 AAG78302 22 AAG78302 22 AAG78307 23 AAF8044 14 AAR39571 4 AAR39571 4 AAR39571 4 AAR39571 11 AAR06554 2 11 AAR06554 2 11 AAR06554 2 11 AAR06554 2 11 AAR07106 4 8 AAP70324 2 11 AAR07118 8 11 AAR07118 8 11 AAR07118 8 11 AAR07118 8 11 AAR07118 8 11 AAR07118 9 13 AAR28572 9 14 AAR39972 9 14 AAR39972	প ভাতন্থাৰৰ থ ৰ তেখন্দ্ৰক্তিত তিন্দ্ৰভাতন্থাৰ্থত ্ৰুন্ন্ৰ্ৰ্ৰ্ণ	Modified castor be	Sequence of Ricinu	Castorbean ricin.	Castor bean ricin	Ricinus communis r	Castor bean prepro		44	Sequence of prepro	Castor bean prepro		44			9	Ricin A from pICI1	á	ď		Ricin A. Syntheti	Castor oil plant a	R. communis agglut	Sequence of Ricin	Ricin agglutinin A	Trichosanthin anti	Amino acid sequenc	Synthetic alpha-tr	Mature alpha-Trich	Trichosanthin (a r			Trichosanthin from	Trichosanthin prot	Encodes chinese cu	ы	Chinese cucumber a
		AAG78304	AAP70326	AAW25787	AAY55892	AAY78592	AAG78301	AAG78302	AAR39570	AAP50166	AAG78300	AAP80164	AAR39571	AAP70325	AAP60240	AAP94793	AAR30722	AAB19265	AAR06554	AAR74176	AAR32430	AAW25143	AAW21706	AAP70324	AAP95648	AAR67359	AAY69048	AAR07518	AAR25573	AAW25140	AAW21703	AAR07514	AAR25572	AAR29272	AAR32986	AAR55129	AAW10468
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24	015 W 4 2 0 0 1 9 2 8 4 2 0 0 1 1 2 E 4 2 0 0 1 2 E 4 2 0																																				

ALIGNMENTS

RESULT 1 AAR37290 ID AAR	LT 1 7290 AAR37290 stand	T 1 290 AAR37290 standard; protein; 267 AA.
ž Z	AAR37290;	
설탕	25-MAR-2003 (1	(updated)
DI	_	(updated)
E S	13-SEP-1993 ((first entry)
DE DE	Ricin A chain.	
X Z	Type II riboso	Type II ribosome-inactivating protein; type II RIP; gelonin;
¥	momordin; immu	momordin; immunoconjugate; autoimmune disease; cell killing; toxin.
×		
SO	Unidentified.	
ğ		
PN	WO9309130-A1.	
설 문	13-MAY-1993.	
×		
PF *	04-NOV-1992;	92WO-US09487.
¥ #	04-NOV-1991;	91US-0787567.
PR	19-JUN-1992;	92US-0901707.
ğ		
PA XX	(XOMA) XOMA CORP.	ORP.
[L]	Berhard SL, B	Better MD, Carroll SF, Lane JA, Lei SP;
i i i i i i	WPI; 1993-167617/20.	17/20.

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61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 181
                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                        The invention covers analogues of Type I RIPs. Ricin is a Type II RIPs whose A chain is homologous to plant type I RIPs. The analogues of the invention have a cysteine available for intermolecular disulphide bonding at an amino acid position corresp. to a position not naturally available for bonding; the cys residue is located in the C-terminal region of the analogue between a position corresp. to amino acid 251 and the C-terminus of ricin A chain. The analogues are pref. joined via a disulphide linkage to a molecule which specifically binds to a target cell, e.g. an antibody fragment.

(Updated on 09-JAM-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                           1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHBIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                     2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
Analogues of type I ribosome inactivating protein - useful as cytotoxic agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in-vivo
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polynucleotide(s) encoding type I ribosome-inactivating proteins
                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                     Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ricin A chain; RTA; ribosome-inactivating proteins; RIPs; cytotoxic therapeutic agents; autoimmune disease; cancer;
                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carroll SF;
                                                                                                                                                                                                                                                                                                                    99.5%; Score 1020; DB 14;
100.0%; Pred. No. 2.7e-100;
Ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Studnicka GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR63902 standard; protein; 267 AA.
                                                               Claim 1; Page 92; 163pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FOYIEGEMRTRIRYNRRS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOYIEGEMRIRIRYNRRS 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     graft-versus-host disease.
                                                                                                                                                                                                                                                                                                                                                   Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carroll SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (updated)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ricin A-chain (RTA)
                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                         267 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (XOMA ) XOMA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ricinus communis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
27-JUL-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR63902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
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61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
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                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 IFPKÖYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maize; proRIP; ribosome inactivating protein; alpha; beta subunit; internal linker; Barley Translation Inhibitor; Trichosanthin; Kicin A-chain; Abrin-A A-chain; Aporin; SIT-1; Luffin A; MAP; Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30; therapeutic toxin; tumour cell targeted; protein synthesis; inhibitor; post-translational modification; cancer; neoplasia; HIV: AIDS; human immunodeficiency virus; acquired immune deficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                            2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                  AAR63902 is the ricin A chain gene product, it is analogous to the ribosome-inactivating proteins (RIPS) described in AAR63903-R63911.
RIPS are the key components of cytotoxic therapeutic agents (CTAS), which include gene fushon products and immunoconjugates. CTAS may be used to selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is
                                                                                                                                                                                                                              desired, such as autoimmune disease, cancer and graft-versus-host
                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                       Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ricin A-chain ribosome inhibitory protein inactive precursor.
                                                                                                                                                                                                                                                                                                                                                                       Indels
are suitable for use as components of cytotoxic
                                                                                                                                                                                                                                                                                                                                   Query Match
99.5%; Score 1020; DB 16;
Best Local Similarity 100.0%; Pred. No. 2.7e-100;
Matches 198; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                              (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW25136 standard; Protein; 290 AA.
                                                  Example 3; Fig 1; 221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 FOYIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 FQYIEGEMRTRIRYNRRS 199
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90US-0535636.
95US-0378761.
95US-0485286.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (updated)
(first entry)
                  therapeutic agents.
                                                                                                                                                                                                                                                                                                    267 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
02-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW25136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122
which
                                                                                                                                                                                                                                                   disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
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(DOWC) DOWELANCO.

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AAP70097 standard; protein; 332 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 FQYIEGEMRTRIRYNRRS 222
                                                                                                                                                                                                                  Walsh TA
                                                                                                   95US-0378761.
                                                                                                                                            90US-0535636
                                                                                                                                                           95US-037B761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                  Morgan AER,
                                                                                                                                                                                                                                              WPI; 1997-309831/28.
                                                                                                                                                                                      (DOWC ) DOWELANCO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290 AA;
                                                                                                   26-JAN-1995;
                                                                                                                              09-DEC-1992;
                                                                                                                                                           26-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-APR-1991
                                          US5635384-A.
                                                                      03-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP70097;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                  AAW25136 represents a Ricin A-chain ribosome inhibitory protein (RIP)
which was engineered to contain a selectively removable internal peptide
linker sequence separating the alpha and betea units of the RIP. When
separated the two units regain activity and are capable of inactivating
cukaryotic ribosomes and hence preventing protein production. Many
different RIPs may be produced with an internal linker including
maize RIP. Trichosanthin, Ricin A-chain, Abrin-A A-chain and
Saporin. The RIPs can be used in the construction of therapeutic
toxins targeted to specific cells such as tumour cells via the
attachment of a targeting polypeptide, e.g. a monoclonal antibody.
A further use is in HIV therapy (see U5486993). There is interest
in expressing RIP recombinantly in host eukaryotic cells, because of
the capacity to provide correct post-translational processing. However,
RIPS effectively inhibit protein synthesis in eukaryotic cells resulting
in cell death. Since the inactive RIP proteins are not cytotoxic to
cukaryotic cells, they can be recombinantly expressed in such cells and
then converted to active RIP proteins.
(Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 ELSNHABELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYIFAFG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 GNYDRLEQLAGNLRENIELGNGPLEEAISALXYYSTGGTQLPTLARSFIICIQMISEAAR 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer; inactivation; eukaryotic ribosome; alpha fragment; beta fragment; inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver; rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.
                                                                   DNA encoding pro-ribosome inactivating proteins - inactive precursors of ribosome inactivating proteins; can be expressed in eukaryotic cells without causing cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.5%; Score 1020; DB 18; Length 290; 100.0%; Pred. No. 3e-100; tive 0; Mismatches 0; Indels 0;
                                                                                                                           Claim 4; Column 91-94; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW21699 standard; Protein; 290 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FQYIEGEMRTRIRYNRRS 199
               Walsh TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOYIEGEMRTRIRYNRRS
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
               Morgan AER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                          WPI; 1997-362934/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ricin A-chain RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                  290 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
26-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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The sequences given in AAW21698-710 represent Ribosome Inactivating Proteins (RIP's), which may be used in the construction of the proteins proteins (RIP's), which may be used in the construction of the proteins in the invention. The proRIP has a selectively removable, internal peptide linker. The precursor sequence is incapable of inactivating eukaryotic ribosomes, but can be converted by removal of the linker into a protein having alpha and beta fragments and being capable of inactivating eukaryotic ribosomes. RIPs are potent inhibitors of eukaryotic protein synthesis. They possess a highly specific N-glycosidase activity which cleaves the glycosidic bond of adenine 4324 of rat liver ribosomal 285 RNB. RIP's selectively inhibit cellular proliferation of cells, e.g. cancer cells and HIV-infected T cells. The inactive proRIP proteins make it possible to provide protein synthesis inhibitors with uses in practical and improved ways not before possible. The RIP can be used to make cytotoxic conjugates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
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/note= "Position of possible insertion of internal
peptide linker sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inactive precursor of maize ribosome-inactivating protein - also
chimeric ribosome-inactivating protein precursors containing
internal linker sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Best Local Similarity 100.0%; Pred. No. 3e-100;
Matches 198; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Column 91-94; 121pp; English.
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/note="A-chain" 315..332 /note="B-chain"

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Region
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ID AAP9
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AC AAP9
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DT 25-1v
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                                                                                                                                                                                                                                                                                                                                             ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 121
                                                                                                                                                                                                                                                                                                                                                                               GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 181
                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                       36 IPPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 95
                                                                                                                                                                                                                                                                                                          2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence of Ricinus communis castor beans ricin toxin (RT or ricin)
                                                                                                                                                                                 N\text{-}terminal methionine free proteins prodn. - by using host transformed with vector to express a methionine-amino-peptidase
                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                            Ricin A may be produced in a form which lacks an N-terminal Metusing Met-aminopeptidase from E.coli.
                                                                                                                                                                                                                                                                       / Match 99.5%; Score 1020; DB 8; Length 332; Local Similarity 100.0%; Pred. No. 3.6e-100; Hes 198; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lectin; toxin protein; cytotoxic; cytostatic; castor bean;
                                                                                                                                        Chang SY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP70838 standard; protein; 332 AA
                                                                                                                                        Chang S,
                                                                                                                                                                                                            Disclosure; Fig. 4; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1..32
/note="Leader"
33..302
                                                                                                                                                                                                                                                                                                                                                                                                                  FOYIEGEMRIRIRYNRRS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                  FOYIEGEMRIRIRYNRRS 233
        Ricin A; Met-aminopeptidase.
                                                                            86EP-0307242.
                                                                                             86US-0860330.
85US-0778414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A protein encoded by pRA123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003 (updated)
18-FEB-1991 (first entry)
                                                                                                                                       Benbassat A, Bauer KA,
                                                                                                                                                         WPI; 1987-110172/16.
                                                                                                                      (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                        332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ricinus communis.
                        Escherichia coli
                                                                                                                                                                N-PSDB; AAN70152
                                                                            19-SEP-1986;
                                                                                             06-MAY-1986;
                                                                                                      20-SEP-1985;
                                                           22-APR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plant toxin
                                         EP219237-A.
                                                                                                                                                                                                                                                        Sequence
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Matches
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The full-length sequences encoding ricin A (AAN70520), ricin D (AAN70525), putative ricin E (AAN70526) and RCA (AAN70524) in precursor form were obted. using messenger RNA to obtain a cDNA library, and then probing the library to retrieve the desired cDNA inserts. The library was probed using the 35-mer given in AAN70514. Figure 4 (see AAN70520, AAN70522), shows the nucleotide sequences of three plasmids contg. cDNA inserts obtain a cDNA library for sequences encoding ricin B using the probing a cDNA library for sequences encoding ricin B using the probing a AAN70517. The cDNA untagenesis may be used to place an ATG start codon and a HindIII site at the beginning of the mature protein (see AAN70518). The coding sequences of the inserts can be ligated into expression vectors contg. the PhoA promoter-operator and leader sequence (AAN70523) and sustable retroregulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 IPPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New non-glycosylated ricin precursor and toxin etc. - are prepd.
by recombinant DNA procedures with specific isolation steps for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.5%; Score 1020; DB 8; I
100.0%; Pred. No. 3.6e-100;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP95639 standard; protein; 332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Fig 1; 112pp; English.
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                                                                                                                               86EP-0308877.
                                                                                                                                                                                                 86US-0837583.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             purer and soluble prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (updated)
(updated)
                                                                                                                                                                                                                                                                                           (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1987-265177/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                               (CETU ) CETUS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAN70519
                                                                                                                               13-NOV-1986;
                                                                                                                                                                                              17-MAR-1986;
                                                              23-SEP-1987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
31-OCT-2002
EP237676-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                            Piatak M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP95639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
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182 FQYIEGEMRTRIRYNRRS 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    94WO-US07919
                                                                                                               (updated)
(first entry)
                                                                                                                                            Anti-cataract immunotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gould RM, Kelleher PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-082036/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      554 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ85386.
                                                                                                              25-MAR-2003
31-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                            WO9503828-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                09-FEB-1995.
                                                                                                                                                                                                        Synthetic.
                                                                                           AAR70827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                   Peptide
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                                                   RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 IFPKQYPIINFTTAGATVQSYTNPIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                             Recombinant vectors expressing ricin chains or diphtheria toxin -used for prodn. of new immunotoxin conjugates with monoclonal antibodies, having high cell specificity and good extracellular stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid RA123 (ATCC No. 39799) carries the entire coding sequence for ricin A, as well as codons for 12 AAs joining the A to the B chain. Following modification for ease of manipulation the plasmid was used to construct expression vectors which express the conjugates in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                      Kaplan D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.5%; Score 1020; DB 10; Length 332; 100.0%; Pred. No. 3.6e-100; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                    Greenfield L, Nitecki D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PR field.)
                                       Plasmid pRA123; ricin-A; ricin-B; cytotoxicity.
                    Ricin A encoded by insert from plasmid pRA123.
                                                                                                  ...35
label= leader sequence
                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Fig 14; 54pp; English.
                                                                                                                                                                                                                                                                                                                                   Gelfand D, Lawyer FC, Horn G,
                                                                                                                      36..302
/label=A-chain
                                                                                                                                                            315..332
/label=B-chain
                                                                                                                                         103..314
/label=linker
                                                                                                                                                                                                                                                             84US-0578121.
84US-0578122.
84US-0648759.
84US-0653515.
                                                                                                                                                                                                                                 89EP-0201162.
                                                                                                                                                                                                                                                     84US-0578115.
 13-AUG-1990 (first entry)
                                                                                                                                                                                                                                                                                                                CORPORATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198; Conservative
                                                                                                                                                                                                                                                                                                                                                                 WPI; 1989-286959/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 AA;
                                                           Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAN91281.
                                                                                                                                                                                                                                                                                                              (CEIU ) CEIUS
                                                                                                                                                                                                                                19-JAN-1989;
                                                                                                                                                                                                                                                    08-FEB-1984;
                                                                                                                                                                                                                                                                                  07-SEP-1984;
20-SEP-1984;
                                                                                                                                                                                                                                                               08-FEB-1984;
                                                                                                                                                                                                                                                                        09-FEB-1984;
                                                                                                                                                                                                             04-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  host cells.
                                                                                                                                                                                          EP335476-A.
                                                                                                                                                                                                                                                                                                                                             Piatak MJ;
                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122
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                                                                                                 Peptide
                                                                                                                     Peptide
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                                                                                                                                                            Peptide
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The immunotoxin given in AAR70827 comprises the heavy and light chain variable regions of anti-lens epithelium 19G3 MAb 4197X linked to intimina, and a hexa-histidine tag. The DNA construct encoding the immunotoxin was expressed from pHB19 in E. coli. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      Immunotoxin, heavy chain, light chain, variable region, antibody,
ricin-A, cytostatic, cataract, lens opacification, epithelial cell;
pHB19, 4197X; monoclonal antibody; MAb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New single chain immuno:toxin - binds specifically to epithelial cells, for inhibiting development of sec. cataracts after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28..145
/label= HEAVY
/note= "MAD 4197X heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               //abe.
169.274
/label= LiGHT
/~~*e= "WAb 419% light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wood MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Sig_peptide
/note= "phoA signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            549..554
/label= TAG
/note= "hexa-histidine tail"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wallace TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                              AAR70827 standard; Protein; 554 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          extra:capsular cataract extraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HOUS-) HOUSTON BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig.4; 68pp; English.
216 FQYIEGEMRTRIRYNRRS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148..166
/label= LINKER
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The sequence relates to the amino acid sequence of a modified preproricin protein encoded by AAI64145. The invention relates to a novel toxin (e.g. ricin) based antiviral agent which is toxic to virus-infected
                                                         156 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 215
              96 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Proricin consists of the ricin A chain, a linker peptide, and the ricin B chain. Proricin is proteolytically cleaved between the A chain and the linker to yield mature ricin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel composition comprising toxin e.g., ricin based antiviral compound useful for treating viral infections such as human immunodeficiency virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
Castor bean plant; preproricin; ricin; A chain; B chain; human immunodeficiency virus infection; HIV; toxin; antiviral agent; retroviral infection; anti-HIV; virucide; viral protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296..297
/label= HIV_protease_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                  Chimeric - Ricinus communis
Chimeric - Human immunodeficiency virus type 2.
                                                                                                                                                                                                                                                                                    Modified castor bean preproricin (SEQ ID 10).
                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Signal_peptide
25..565
/label= Proricin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292..303
/label= Linker_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'label= Ricin A_chain
'note= "N-glycosidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 59-63; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            cocation/Qualifiers
                                                                                                                                                                                                 AAG78304 standard; Protein; 565 AA.
                                                                                                 182 FOYIEGEMRIRIRYNRRS 199
                                                                                                                            216 FOYIEGEMRTRIRYNRRS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BECH-) BECHTEL BWXT IDAHO LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-FEB-2000; 2000US-0182759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-FEB-2001; 2001WO-US05282
                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25..291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Keener WK, Ward TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-581908/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAI64145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200160393-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cleavage-site
                                                                                                                                                                                                                                                        27-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-AUG-2001.
                                                                                                                                                                                                                            AAG78304;
                                                                                                                                                                                                                                                                                                                                                                                                                Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
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              GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 181
                                                     ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 121
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 61
                                                                                                                                   398 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ricin D (see corresp. AAN90068) found on the EcoRI-HindIII fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of DNA from Ricinu communis, Zanibariensis variety. Patent discloses many modifications of ricin in which the lectin binding thoreton of the B chain is diminished or removed, and conjugation to toxins to eliminate cell binding.

(Updated on 25-MAR-2003 to correct PA field.)

(Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                           Ricin D; Ricinus communis; caster beans; Zanibariensis variety; modified; lectin binding removed; reduced cell binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.5%; Score 1020; DB 10; Length 562; 100.0%; Pred. No. 7.4e-100; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified ricin molecules and toxin conjugates - in which the lectin binding function of the B chain is removed or diminished to reduce cell binding.
                                                                                                                                                                                                                                                                 AAP90079 standard; protein; 562 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; fig 1; 51pp; English.
                                                                                                                                                                                           458 FOYIEGEMRTRIRYNRRS 475
                                                                                                                                                                                                                                                                                                                                                                                                                                        Ricinus communis (caster beans)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87US-0124735.
                                                                                                                                                                    FOYIEGEMETRIRYNRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88WO-US04238.
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                         (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1989-178366/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brown EL, Jones S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                562 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAN90068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-NOV-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO8904839-A.
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Matches 198;
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                                                                                                                                                                                                                                                                                                                                        01-NOV-1989
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                                                     62
                                                                                                                                                                    182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                  Ricin D.
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cells, but non-toxic to uninfected cells. The invention has anti-HIV and valuated activities. The agent is able to enter all HIV susceptible cells, and not just cells known to act as host cells for the virus. The antiviral agent remains inert in a cell unless the cell is infected with the HIV virus, where the viral protease activates it. Ricin's mechanism of action is through inactivation of cellular ribosomes and enhancement of binding of the antiviral agent to galactose residues on cell surfaces, and its cellular internalisation. The invention is useful infections, especially retroviral infections and other viral activated in viral particles or early-stage infected cells, killing the cells upon infection and effectively preventing the inregration of the viral genome into the host genome thereby preventing the latency/rebound
                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 ELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNYDRLEQLAGNLRENIELGNGPLEEAISALXYYSTGGTQLPTLARSFIICIQMISEAAR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICTQMISEAAR 204
                                                                                                                                                                                                                                                                                                                                                                                        84
                                                                                                                                                                                                                                                                                                                                                                           25 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                      2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                    99.5%; Score 1020; DB 22; Length 565; 100.0%; Pred. No. 7.5e-100; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lectin; toxin protein; cytotoxic; cytostatic; castor bean;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of Ricinus communis (castor bean) Ricin toxin (RT or ricin) B precursor encoded by pRT38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAP70326 standard; Protein; 576 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "A-chain"
315..576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "B-chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 FQYIEGEMRTRIRYNRRS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 FQYIEGEMRTRIRYNRRS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "leader"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86US-0837583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86EP-0308877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (updated)
(first entry)
                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36..302
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                                                                                                                                                                                                                                                    565 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-MAR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-SEP-1987,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plant toxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP70326;
                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
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The full length sequences encoding ricin A (AAN70520), ricin D (AAN70525) putative ricin E (AAN70526) and RCA (AAN70524) in precursor form were obtained, using the messenger RNA to obtain a CDNA library, and then probing the library to retrieve the desired CDNA inserts. The LAM70521, AAN70521, Shows the nucleotide sequences of three plasmids containing cDNA inserts obtained by probing a cDNA library for sequences encoding ricin B using the probe in AAN70517. The CDNA inserts can be placed into expression vectors. Site-directed mutagenesis may be used to place an ATG start codon and a Hindlil site at the beginning of the mature protein, (see AAN70518). The coding sequences of the inserts can be ligated into expression vectors containing the PDOA promoter-operator and leader sequence (AAN70523) and suitable retroregulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 GNYDRLEQLAGNLENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                          New non-glycosylated ricin precursor and toxin etc. - are prepd.
by recombinant DNA procedures with specific isolation steps for
purer and soluble prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ricin, cytotoxin, hybrid protein, cell delivery; cell binding ligand; translocation domain; diphtheria toxin B'; interleukin-2; T-cell lymphoma; organ rejection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 99.5%; Score 1020; DB 8; Length 576; Best Local Similarity 100.0%; Pred. No. 7.7e-100; Matches 198; Conservative 0; Mismatches 0; Indels Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                     Disclosure; Fig 14(1-2); 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Sig_peptide
36..302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW25787 standard; Protein; 576 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 FOYIEGEMRIRIRYNRRS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 FOYIEGEMRIRIRYNRRS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (updated)
(first entry)
                                                      WPI; 1987-265177/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       576 AA;
                                                                    N-PSDB; AAN70526.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Castorbean ricin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-2003
27-MAR-1998
                Piatak M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW25787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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Peptide
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ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ricin-dipthheria toxin B'.interleukin-2 gene that was expressed in ricin-dipthheria toxin B'.interleukin-2 gene that was expressed in E. coli. The hybrid protein can be isolated and used to treat conditions involving over-production of cells bearing 112 receptors, such as certain T-cell lymphomas and organ transplant rejection crises. The hybrid inactivates ribosomes in cells bearing 112 receptors, resulting in cessation of protein synthesis and death of target cells. Claimed hybrid proteins comprise a translocation of meanin and a cell binding domain from e.g. a hormone, growth factor of meanin and a cell binding domain from e.g. a hormone, growth factor. The hybrid molecules can be used for the cells toxin. The hybrid molecules can be used for the that the hybrid will be effective in relatively low doses, since a high proportion of the substance of interest will be taken into the targeted cells. The hybrid molecules can be manufactured as a single hybrid recombinant protein, permitting reproducibility, consistency, and the precise control of composition.

(Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprise a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This polypeptide comprises the castorbean cytotoxin, ricin. DNA (see AAT91638) encoding the enzymatic A domain and a portion of the A-to-B linker peptide of ricin was used to construct a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New hybrid molecules for delivery of agents to cells - cc
binding domain of a cell binding ligand and a portion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.5%; Score 1020; DB 18;
100.0%; Pred. No. 7.7e-100;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Fig 11A-B; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translocation domain of a protein
               /label= Linker
315..576
/label= B-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FQYIEGEMRTRIRYNRRS 199
                                                                                                                                                                                           91US-0722484.
84US-0618199.
85US-0726808.
85US-0742554.
89US-0456095.
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Best Local Similarity 100.0
Matches 198; Conservative
303..314
                                                                                                                                                                                                                                                                                                                                           (SERA-) SERAGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-470103/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                576 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAT91638
                                                                                                                                                             04-AUG-1993;
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                                                                                                                                                                                               27-JUN-1991;
                                                                                                                                                                                                                                   25-APR-1985;
                                                                                                                                                                                                                                                      07-JUN-1985;
                                                                                     US5668255-A
                                                                                                                         16-SEP-1997
                                                                                                                                                                                                                                                                     22-DEC-1989
                                                                                                                                                                                                                                                                                      4-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                               Murphy JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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Peptide
                                    Jomain
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Recombinant, hybrid, binding domain, ligand; animal cell, diphtheria, translocation domain, botulinum; neurotoxin, ricin, cholera, tetanus; shiga-like toxin; pertussis, translocation; cytoplasmic membrane, HIV; cytosol; therapy; genetic deficiency diseases; enzyme; co-factor; poison; adipocyte; cancer; virus; infection; antibody.
                                                                                                                                                                                                                                                                                                                                                                                      Recombinant DNA molecule encoding a three part hybrid protein used in the treatment of Aids and genetic deficiency diseases -
                                            AAY55892 standard; Protein; 576 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Fig 11; 31pp; English
216 FQYIEGEMRTRIRYNRRS 233
                                                                                                                                                                                                                                                       84US-0618199.
91US-0722484.
85US-0726808.
85US-0742554.
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                                                                                                                                                                                                                                                                                             89US-0456095
                                                                                                                                                                                                                                                                                                     90US-0538276
                                                                               (first entry)
                                                                                                  Castor bean ricin toxin.
                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-632431/54.
                                                                                                                                                                                                                                                                                                                       (SERA-) SERAGEN INC.
                                                                                                                                                                         Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAZ30663.
                                                                               15-FEB-2000
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27-JUN-1991;
25-APR-1985;
                                                                                                                                                                                                                              1995;
                                                                                                                                                                                          US5965406-A.
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                                                                                                                                                                                                                                                                                                      14-NUT-1990;
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                                                                                                                                                                                                                                                                                    07-JUN-1985
                                                                                                                                                                                                                                                                                             22-DEC-1989
                                                                                                                                                                                                                                                                                                                                          Murphy JR;
                                                             AAY55892;
                         RESULT 13
                                  AAY55892
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The invention relates to a recombinant DNA molecule encoding a hybrid protein comprising three parts: (a) the first part comprises a portion of the binding domain of a cell-binding polypeptide ligand allowing the hybrid protein to bind to an animal cell; (b) the second part comprises a portion of a translocation domain of a naturally occurring protein selected from diphtheria toxin, botulinum neurotoxin, ricin, cholera toxin, LT toxin, Siga-like toxin, pertussis toxin and tetanus toxin, which translocate the third part of the across the cytoplasmic membrane into the cytosol of the cell; and (c) the third part comprises a polypeptide entity to be introduced into the cell, which is non-native to the naturally occurring protein of (b). This sequence represents the castor bean ricin toxin sequence for use in generating the hybrid of the therapy to affected cells, allowing them to function properly and allewiate or cure the disease. The hybrid is especially used in treating generation defined calls, allowing them to affected cells an enzyme contains the contai particular enzyme or a scarce precursor or cofactor, to directing toxins or other poisons to destroy particular cells (such as adipocytes, cancer cell, or virus infected-cells), to counteracting viral infections such as HIV, by introducing appropriate antibodies to viral proteins. It is also involved in the process of getting non-therapeutic substances such as detectable labels into cells. supplying the missing function, to supplementing cellular levels of a

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19

121

576 AA; Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ricin, toxin, hybrid protein, translocation domain, cell destruction, cell binding domain, genetic deficiency disease; cell targetting, cancer, adipocyte, enzyme delivery; anti-viral, HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents the Ricinus communis ricin protein sequence. The toxin can be included in the hybrid protein of the invention and used to destroy or modify the cell that the hybrid protein is targeted to. The hybrid protein comprises a first part which is a portion of the binding domain of a cell-binding ligand, effective to cause the hybrid molecule to bind to a cell of an animal. The second part comprises a portion of a translocation domain of a naturally occurring protein (e.g. the translocation domain of diphtheria toxin) the second part translocates the third part across the cytoplasmic membrane and into the cytosol of
                                                                                                                          121
                                                                                                                                                         155
                                                                                                                                                                                      181
                                                                                          95
                                                             61
                                                                                                                                           ELSNHAELSVTLALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                           156 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                       ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                   GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                           2 IFPKOYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                        36 IFPKOYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New two-part hybrid protein comprising a translocation domain and a cell-binding domain, for treating genetic deficiency diseases, cancer
                                Gaps
                              0;
 Length 576;
                              0; Indels
Score 1020; DB 20;
Pred. No. 7.7e-100;
        100.0%; Pred. w..
                                                                                                                                                                                                                                                                                                                                                                                                                                               Ricinus communis ricin protein sequence
                                                                                                                                                                                                                                                                                                                                                      AAY78592 standard; Protein; 576 AA.
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                                                                                                                                                                                                                                                                          216 FOYIEGEMRIRIRYNRKS 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91US-0722484.
85US-0726808.
85US-0742554.
89US-0456095.
99.58;
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                             Matches 198; Conservative
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                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and HIV infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ricinus communis.
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                                                                                                                                                                                                                                             182
                                                                                                                                                                                                                                                                                                                                                                                       AAY78592;
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Query Match
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the cell. The third part comprises a chemical entity to be introduced into the cell, where each of the first and third part is non-native with crespect to naturally occurring protein, and the covalent bond attaching the second and third part is cleavable. The toxin represented by the protein. The cell binding domain binds to a specific cell and the translocation domain transfers the hybrid molecule across the cell membrane into the cytosol. The third part of the protein, linked to the translocation domain through a cleavable bond, can then carry out its function. The hybrid molecules are useful for treating genetic deficiency diseases by delivering to affected cells an enzyme supplying the missing function, to supplement cellular levels of a particular enzyme or a coarce precursor or cofactor, to direct toxins or other poisons to destroy particular cells (such as adipocytes, cancer cells, or virus-infected cells), and to counteract viral infections such as HIV by introducing into appropriate cells antibodies to viral proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICLQMISEAAR 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Linker_peptide
/note= "Cleaved during activation of ricin"
315..515.5
/label= Ricin_B_chain
/note= "Galactose/N-acetylgalactosamine-binding lectin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                               2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Castor bean plant; preproricin; ricin; A chain; B chain; human immunodeficiency virus infection, HIV; toxin; antiviral agent; retroviral infection; anti-HIV; virucide activity; viral protease.
                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                      Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                      99.5%; Score 1020; DB 21;
100.0%; Pred. No. 7.7e-100;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Castor bean preproricin protein (SEQ ID 2).
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/label= Signal peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36..302
/label= Ricin A chain
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Matches 198; Conservative
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                                                                                                                                                                                                                                                                                                                                576 AA;
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us-10-083-336a-5.rag

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The sequence relates to preproricin protein encoded by the DNA sequence given in AAI64138. The invention relates to a novel toxin (e.g., ricin) based antiviral agent which is toxic to virus-infected cells, but non-toxic to uninfected cells. The invention has anti-HIV and virucide activities. Its mechanism of action is through inactivation of cellular incomes and enhancement of binding of the antiviral agent to galactose residues on cell surfaces, and its cellular internalisation. The invention is useful for treating human immunodeficiency virus infection and other viral infections, especially retroviral infections. The antiviral agent is activated in viral particles or early-stage infected cells, killing the cells upon infection and effectively preventing the integration of the viral genome into the host genome thereby preventing the latency/rebound problem. The agent enters all HIV susceptible cells, and not just cells known to act as host cells for the virus. The antiviral agent remains inert in a cell until degraded in it, unless the cell is infected with the virus, where the viral protease activates it.
                                                                                                                                                                                                                                                      Novel composition comprising toxin e.g., ricin based antiviral compound useful for treating viral infections such as human immunodeficiency virus infection.
                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 50-54; 66pp; English.
                                                                                        (BECH-) BECHTEL BWXT IDAHO LLC
15-FEB-2001; 2001WO-US05282.
                                            16-FEB-2000; 2000US-0182759.
                                                                                                                                                                                 WPI; 2001-581908/65.
N-PSDB; AAI64138.
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96 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 155 122 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 181 156 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 215 62 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 121 2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 0; Gaps 99.5%; Score 1020; DB 22; Length 576; 100.0%; Pred. No. 7.7e-100; tive 0; Mismatches 0; Indels 0 FOYIEGEMRIRIRYNRRS 199 216 FOYIEGEMRIRIRYNRKS 233 Best Local Similarity 100.0 Matches 198; Conservative Query Match Пþ QQ g ð à δ

Search completed: February 10, 2004, 16:22:26 Job time : 34.9288 secs

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1 MIFPKQYPIINFTTAGATVQ.....ARFQYIEGEMRTRIRYNRRS 199
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Patent No.
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1: /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
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6: /cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-485-286-27
524666-4
US-08-318-303-16
US-09-538-793D-61
US-09-538-873-1
US-08-378-761A-77
US-08-488-113B-6
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US-08-356-786-10
US-07-901-707-1
US-07-988-430-1
US-08-425-336-1
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US-08-477-484-1
US-08-646-360-1
US-08-839-765-1
US-09-610-838-1
US-09-610-838-1
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Maximum Match 100%
Listing first 45 summaries
                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Database :

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342 3442 3442 3442 3442 3442 3423 3423	PERSONAL PROPERTY AND AND AND AND AND AND AND AND AND AND	786 786 19 19
22 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 Sequence No Sequence	; MOLECULE US-08-356-786 Query Match Best Local Matches 19

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63 VELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAF 122
                                      121 GGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAA 180
                                                                       123 GGNYDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAA 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19920619
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent'n Palaco
                                                                                                                                                                                                                                                         Sequence 1, Application US/07901707 Patent No. 5376546
                                                                                                                    181 RFQYIEGEMRTRIRYNRRS 199
                                                                                                                                                        183 RFOYIEGEMRTRIRYNRRS 201
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(312) 984-5750
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AMINO ACID
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Best Local Similarity 100.0
Matches 198; Conservative
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MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                            61 VELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAF 120
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1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFIL 60
                                 1 MIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFIL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biosynthetic Binding Protein for Cancer
Marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R. Pitcher, Testa, Hurwitz, & Thibeault
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100.0%; Pred. No. 1.7e-111;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829
REGISTRATION NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07/831,967
                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 10, Application US/08356786; Patent No. 5877305
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
ITLLE OF INVENTION: Biosynthetic
ITLLE OF INVENTION: Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                   181 RFQYIEGEMRTRIRYNRRS 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/83
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFRAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.(
Matches 199; Conservative
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MOLECULE TYPE: protein
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CITY: Boston
STATE: Massachusetts
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Edmund
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US-08-356-786-10
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APPLICANT: Betrer, Marc D.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Steve F.
APPLICANT: Lane, Julie A.
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
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GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 181
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APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UNN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787 F27
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 04-NOV-1991
ATTORNEY AGENT INFORMATION:
NAME: Meyers, Thomas C.
REGISTRATION NUMBER: P-36,989
REFERENCE/DOCKET NUMBER: 31394
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-6300
TELEX: 25-3856
INFORMATION FOR SEC IN NO: 1:
SECUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                          Sequence 1, Application US/08425336 Patent No. 5621083
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                                                                                       182 FQYIEGEMRTRIRYNRRS 199
                                                                                                                                181 FOYIEGEMRTRIRYNRRS 198
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amino acid
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ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STREET: 65.C.
CITY: Chicago
TT: Illinois
TTS: TTS
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Best Local Simi
Matches 198;
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                                                                                                                                                                                                                                                                           APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lene, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
CORRESPONDENCE ADDRESS:
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                           121 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICTOMISEAAR 180
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0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Two First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patentin Release #1.0, Version #1.25
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CLASSIFICATION: 435
PRICR APPLICATION: 435
PRICR APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRICR APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5416202and, Greta E.
REGISTRATION NUMBER: 35302
REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
TELECHONE: (312) 346-5750
TELEPHONE: (312) 984-9740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUCKENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,430
FILING DATE: 19921209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                             US-07-988-430-1
; Sequence 1, Application US/07988430
; Patent No. 5416202
                                                                 182 FQYIEGEMRTRIRYNRRS 199
                                                                                                         181 FOYIEGEMRTRIRYNRRS 198
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 267 amino acids
AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Bernham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
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                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary Mains Gary
TITLE OF INVENTION: Immunotoxins Comprising Ribsome-Inactivating
TITLE OF INVENTION: Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.5%; Score 1020; DB 1; Length 267; ilarity 100.0%; Pred. No. 2.3e-111; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 140
CORRESONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6310 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 18-APR-1995
CLASSIFCATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
                              62 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 121
                                                                                                                           122 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studinka, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.5%; Score 1020; DB 1; Length 267;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-UNN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 09-DEC-1992
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION DATA: 05-DEC-1992
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA: 05-DEC-1992
RIOR APPLICATION DATA: 05-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCANICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
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APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRICA APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-NAY-1993
PRICA APPLICATION NUMBER: US 08/064,691
PRICA APPLICATION NUMBER: US 07/988,430
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08477484B
Patent No. 5756699
GENERAL INFORMATION:
                                                                                                                                                                                                                             182 FQYIEGEMRTRIRYNRRS 199
                                                                                                                                                                                                                                                                           181 FQYIEGEMRTRIRYNRRS 198
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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US-08-477-484B-1
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                         121 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 180
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Sequence 1, Application US/08488113B
Patent No. 5744580
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Proteins
VUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.5%; Score 1020; DB 1; Length 267; 100.0%; Pred. No. 2.3e-111; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,113B
FILING DATE: US/08/488,113B
FILING DATE: US/08/488,113B
FILING DATE: US/08/488,113B
FILING DATE: US/08/488,113B
FILING DATE: US/08/48,136
FILING DATE: US/08/48;
RAPPLICATION NUMBER: US/08/4691
FILING DATE: L2-MAY-1993
FILING DATE: US-MAY-1993
FILING DATE: US-MAY-1993
FILING DATE: US-DATA:
APPLICATION NUMBER: US/1988,430
FILING DATE: US-DEC-1992
FILING DATE: US-DEC-1992
FILING DATE: US-DEC-1992
FILING DATE: US-DEC-1992
FILING DATE: US-DEC-1992
FILING DATE: US-DEC-1992
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FILING DATE: US-DEC-1992
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REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
TELECOMMUNICATION INFORMATION:
TELECHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
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FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                          182 FOYIEGEMRIRIRYNRRS 199
                                                                                                                      181 FOYIEGEMRTRIRYNRRS 198
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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STREET: 500
CITY: Chicago
TH: Illinois
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Best Local Similarity
Matches 198; Conserva'
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US-08-488-113B-1
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US-08-646-360-1
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US-08-839-765-1
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                                                                                                     1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
                                                               2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILV
                        0; Gaps
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APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
                        0; Indels
100.0%; Pred. No. 2.3e-111;
tive 0; Mismatches 0;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
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FILING DATE: 12-MAY-1993
FAROR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
                                                                                                                                                                                                                                                                                                                          182 FQYIEGEMRIRIRYNRRS 199
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
                      Matches 198; Conservative
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Best Local Similarity
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STATE: Illinois
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                                                                                        99.5%; Score 1020; DB 2; Length 267; 100.0%; Pred. No. 2.3e-111; tive 0; Mismatches 0; Indels
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REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
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APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/839,765
FILING DATE: 15-APR-1997
CLASSIFICATION: 530
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09-DEC-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1, Application US/08839765; Patent No. 6146631
                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 FQYIEGEMRTRIRYNRRS 199
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PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                                                                     Query Match
Best Local Similarity 100.0
Matches 198; Conservative
TOPOLOGY: linear MOLECULE TYPE: protein
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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MEDIUM TYPE: Floppy
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STREET: Suc
CITY: Chicago
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181 FQYIEGEMRTRIRYNRRS 198
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                : 267 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 198; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                62 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 121
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Patent No. 6146850
RENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Garroll, Stephen F.
TILLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins
TITLE OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                Query Match 99.5%; Score 1020; DB 3; Length 267; Best Local Similarity 100.0%; Pred. No. 2.3e-111; Matches 198; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
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APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA: 12-MAY-1993
FILING DATE: 12-MAY-1993
PRIOR APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA: US 07/981,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA: US 07/901,707
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FILING DATE: 19-JUN-1992
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SYSTEM: PC-DOS/MS-DOS
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TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
TELEPHONE: 312/707-8889
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: C
                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
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STREET: 500 mc..
CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                     US-08-839-765-1
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US-09-136-389-1
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61 ELSNHABELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
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APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.5%; Score 1020; DB 3; L. 100.0%; Pred. No. 2.3e-111; tive 0; Mismatches 0;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,838
FILING DATE: 06-JUL-2000
CLASSIFICATION:
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STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
PRIOR APPLICATION DATA:
APPLICATION NUBBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAS, JANGER: 32,918
REGISTRATION NUMBER: 200-70.P4
TELECHONICATION INFORMATION:
TELECHONE: 312/707-8889
TELEFAX: 312/707-8155
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APPLICATION NUMBER: US/09/136,389
FILING DATE: 18-ANG-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
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Patent No. 6376217
GENERAL INFORMATION:
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (312) 984-9740
TELEK: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 267 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-bing
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 121
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Preq. ...
FILING DATE: 14-00.

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY AGENT INFORMATION:
NAME: MCNICOLIAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAM: 312/707-8889
TELEFAM: SEG ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application PC/TUS9209487 GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 267 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 198; Conservative
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STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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Facence 27. Application US/08378761A

Patent No. 5635384

GENERAL INFORMATION:
APPLICANT: MALSH, TERENCE A

APPLICANT: MCTAY D

APPLICANT: MCRAN, ALICE ER

TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE

TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF

TITLE OF INVENTION: USING

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ELSNHABLSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
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                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: PCT/US92/09487
FILING DATE: 19921104
                                                                                               FILING DATE: 19921104
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UW-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
RAME: NOLANG, GREEA E.
REGISTRATION NUMBER: 35302
REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
PC-DOS/MS-DOS
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STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
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Search completed: February 10, 2004, 16:29:32
 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                 290 amino acids
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                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                     ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-485-286-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALICE E.R.
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PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
USING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 ELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYTFAFG 121
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APPLICATION NUMBER: US/08/485,286
PatentIn Release #1.0, Version #1.25
               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
FILING DATE: 26-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 27, Application US/08485286
; Patent No. 5646026
; Patent No. 5646026 5646119
                                                 FILING DATE: 26-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 3827;
REFERENCE/DOCKET NUMBER: 3827;
TELECOMMUNICATION INFORMATION:
TELEFONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENČE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONAVILLE ROAD
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 PQYIEGEMRTRIRYNRRS 199
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-
TITLE OF INVENTION: PRECIRSOR
TITLE OF INVENTION: USING
                                                                                                                                                                                                                                            290 amino acids
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 198; Conservative
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MOLECULE TYPE: protein

US-08-378-761A-27
                                                                                                                                                                                                                                                                                  single
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                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS: sin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46268
 SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TITLE OF INVENTION: DNA ENCODING INACTIVE PRECURSOR AND ACTIVE FORMS OF MAIZE RIBOSOME INACTIVATIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: WALSH, TERENCE A.; HEY, TIMOTHY D.; MORGAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.5%; Score 1020; DB 6; I 100.0%; Pred. No. 2.6e-111; Live 0; Mismatches 0;
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FILING DATE: 11-JUN-1990
                                                               38272B
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33621.
REFERENCE/DOCKET NUMBER: 3827.
TELECOMMUNICATION INFORMATION:
TELEPHORE: (117) 337-4846
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
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Job time : 12.5063 secs

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February 10, 2004, 16:26:46; Search time 25.6679 Seconds (without alignments) 1623.314 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1025
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Seguence 5, Appli	10.	'n	-	Н	7	H	H	Sequence 6, Appli	Ξ	4	80	Sequence 9, Appli	N	39.	٠
ID	US-10-083-336A-5	US-10-083-336A-10	US-10-083-336A-3	US-10-127-890-1	US-10-083-336A-1	US-10-083-336A-7	US-10-282-935-1	US-10-440-796-1	US-10-083-336A-6	US-10-083-336A-11	US-10-083-336A-4	US-10-083-336A-8	US-10-083-336A-9	US-10-083-336A-2	US-09-792-793A-39	
	12	12	12	12	12	12	12	12	12	12	12	12	12	12	10	
Query Match Length DB	199	200	198	267	576	198	267	267	189	190	188	188	185	179	247	
Query Match]	100.0	100.0	99.5	99.5	99.5	98.5	98.5	98.5	93.3	93.3	92.8	91.8	91.2	73.0	33.4	
Score	1025	1025	1020	1020	1020	1010	1010	1010	926	926	951	941	934.5	748	342	
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Sequence 6, Appli	Sequence 39, Appl	4	m	m	m	34	4	7	Sequence 2, Appli	ω	e)	110	Sequence 111, App	101	Sequence 99, Appl	107	100		247, A	Sequence 2, Appli	Sequence 102, App	103		10	'n	11		259,	
.2 US-10-127-890-6	US-10-375	ns-	.2 US-10-282-935-3	.2 US-10-440-796-3	$\Omega S = 0$.2 US-10-375-209A-34	US-10-		US-09-347-064-2	US-09-347-064-8	.2 US-10-127-890-5	.2 US-10-127-890-110	0-127-890	.2 US-10-127-890-101	.2 US-10-127-890-99	.2 US-10-127-890-107	.2 US-10-127-890-100	.2 US-10-127-890-106	US-09-765-527-247	US-10	.2 US-10-127-890-102	US-10	.2 US-10-127-890-104	US-10-127-	.2 US-10-074-596-1	.2 US-10-074-596-11		NS-09-765-527-259	US-09-765-527-253
247 1	247 1	289 1	251 1	251 1	247 1	247 1	263 1	263 1	252 9	252 9	248 1	251 1	251 1	251 1	251 1	251 1	251 1	251 1	251 9	251 1	251 1	251 1	251 1	251 1	316 1	507	251 1	293 9	309
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ALIGNMENTS

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US-10-083-336A-5

Sequence 5, Application US/10083336A

Sequence 5, Application US/1008336A

Publication No. US20020181665A1

GENERAL INFORMATION:

APPLICANT: Olson, Mark A

APPLICANT: Byrne, Michael P

APPLICANT: Byrne, Michael P

APPLICANT: Wannemacher, Robert W

TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REPRENCE: PG7422UG (RILD 01-58)

CURRENT APPLICATION NUMBER: US/10/083,336A

CURRENT FILING DATE: 2002-05-21

NUMBER OF SEQ ID NOS: 15
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100.0%; Score 1025; DB 12; Length 199;
Best Local Similarity 100.0%; Pred. No. 1.5e-109;
Matches 199; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT; ORGANISM: Ricinus communis US-10-083-336A-5
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                                                                                                                                                                                                                                                                                                                NUMBER SOFTWARE: Pater
SEQ ID NO 5
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121 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICTQMISEAAR 180
                                                                                                              61 ELSNHABLSVTLALDVTNAYVVCYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
                                                                                                                                                                      122 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 181
     1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/646,360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: McNicholas, Janet M. REGISTRATION NUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/10127890
Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
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CORRESPONDENCE ADDRESS:
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Publication No. US2003018165A1
GENERAL INFORMATION
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Minlard, Charles B
APPLICANT: Mannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: F67452US0 (RIID 01-58)
CURRENT PILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                              APPLICANT: Olson, Mark A
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Michael P
APPLICANT: Wannemacher, Robert W
APPLICANT: Wannemacher, Robert W
APPLICANT: Wannemacher, Robert W
APPLICANT: Wannemacher, Robert W
APPLICANT: Wannemacher, Robert W
APPLICANT: Wannemacher, Robert W
APPLICANTON: Right Vaccine and Methods of Making and Using Thereof
FILE REPERENCE: P67452USO (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
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ilarity 100.0%; Pred. No. 5.5e-109;
Conservative 0; Mismatches 0;
                                                                                                                                                                Sequence 10, Application US/10083336A Publication No. US20030181665A1 GENERAL INFORMATION:
181 REQYIEGEMRITRIRYNRRS 199
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Best Local Similarity
Matches 198; Conserva
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Best Local Similarity
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LENGTH:

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Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
Proteins
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                                                                                                                                                                               ADDRESSE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
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                                                                       2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 61
                                                                                                                   1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHBIPVLPNRVGLPINQRFILV 60
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APPLICANT: Olson, Mark A
APPLICANT: Milard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452USO (RIID 01-58)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Olson, Mark A
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher; Waccine and Methods of Making and Using Thereof
TITLE OF INVENTION: NABER: US/10/083,336A
CURRENT FILING DATE: 2020-05-21
NUMBER OF SEQ ID NOS: 15
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                              0; Indels
     Pred. No. 8.5e-109;
                              0; Mismatches
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100.0%;
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                              Conservative
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  Best Local Similarity
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LENGTH: 576
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APPLICANT: GHETIE, VICTOR F.
APPLICANT: SMALLSHAW, JOBAN
APPLICANT: SMALLSHAW, JOBAN
APPLICANT: BALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
FILE REFERENCE: UTSD:884US
                                                                                                                                                                                                                                                                                                                                                                                                       64 SNHAELSVTIALDVTNAYVVGYRAGNSAYFFHPDNQEDABAITHLFTDVQNRYTFAFGGN 123
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                                                                                                                                                                                                                           98.5%; Score 1010; DB 12; 100.0%; Pred. No. 7.8e-108;
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ilarity 100.0%; Pred. No. 1.2e-107;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                         100.0%; Pred. ...
CURRENT APPLICATION NUMBER: US/10/083,336A CURRENT FILING DAPE: 2022-05-21 WUMBER OF SEG ID NOS: 15 SOFTWARE: Parentin Ver. 2.1
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CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: 09/538,873
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PRIOR APPLICATION NUMBER: 60/126,826
PRIOR PILING DATE: 1999-03-30
SUMMBER OF SEQ ID NOS: 23
SUFFWARE: PATENTIN VET. 2.1
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Publication No. US20030143193A1
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Best Local Similarity
Matches 196; Conserv
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                                                                                                                                    TYPE: PRT
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                                                                                             SEQ ID NO 7
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APPLICANT: GHETIE, VICTOR F.
APPLICANT: SMALLGHAW, JOAN
APPLICANT: SMALLGHAW, JOAN
APPLICANT: BALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
TITLE OF INVENTION: SYNDROME (VLS)
FILE REPERRENCE: UTSD: 603
CURRENT APPLICATION NUMBER: US/10/440,796
CURRENT APPLICATION NUMBER: US/09/538,873
PRIOR APPLICATION NUMBER: 60/126,826
PRIOR APPLICATION NUMBER: 60/126,826
PRIOR FILING DATE: 1999-03-30
SRIOR FILING DATE: 1999-03-30
SNUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN VEY: 2.1
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YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTIARSFIICIQMISEAARFQ 182
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Publication No. US20030181665A1
GENERAL INFORMATION:
APPLICANT: Olson, Mark A
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Minlard, Charles B
APPLICANT: Minlard, Charles B
APPLICANT: Monemencher, Mobert W
APPLICANT: Monemencher, Mobert W
APPLICANT: Mobert W
APPLICANT: Mobert W
APPLICANT: Mobert W
APPLICANT: Mobert W
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                  Sequence 1, Application US/10440796; Publication No. US20040009148A1; GENERAL INFORMATION:
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US-10-083-336A-6
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US-10-440-796-1
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APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REPERBENGE: 8674520180 (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
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95.0%; Pred. No. 1.2e-101;
tive 0; Mismatches 0;
                                                                                     Score 956; DB 12;
Pred. No. 1.2e-101;
0; Mismatches 0;
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                                                                                          93.3%;
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TYPE: PRT ORGANISM: Ricinus communis
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                                                                                                                                             Matches 189; Conservative
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                                                                                                                    Best Local Similarity
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US-10-083-336A-11
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US-10-083-336A-4
                                               US-10-083-336A-6
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LENGTH: 190
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113 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 172
                                              184 YIEGEMRTRIRYNRRS 199
                                                                                         173 YIEGEMRIRIRYNRRS 188
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US-10-083-336A-2
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P6745208 (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
SOFTWARE: Patentin Ver. 2.1
SEQID NO 8.
                APPLICANT: Olson, Mark A
APPLICANT: Milard, Charles B
APPLICANT: Milard, Charles B
APPLICANT: Milard, Charles B
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT APPLICATION NUMBER: US/10/083,336A
SUFTWARE: Patentin Ver: 2.1
SUGID NO 9: 15
SUGID NO 9: 10.00
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                                                                                                                                                                                                                                                                                                                                                                                          92.8%; Score 951; DB 12; Length 188; 94.9%; Pred. No. 4.5e-101; ive 0; Mismatches 0; Indels 10
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Pred. No. 6.3e-100;
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94.9%;
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Best Local Similarity 94.9
Matches 188; Conservative
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Best Local Similarity 94.9
Matches 186; Conservative
GENERAL INFORMATION:
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Publication No. US20030181665A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Minnemacher, Robert W
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452USO (RIID 01-58)
CURRENT PAPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
                                                                                                APPLICANT: Olson, Mark A
APPLICANT: Olson, Mark A
APPLICANT: Milard, Charles B
APPLICANT: Milard, Charles B
APPLICANT: Mannemacher, Robert W
APPLICANT: Wannemacher, Robert W
APPLICANT: Wannemacher, Robert W
FITLE OF INVENTIONS: Rich Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452USO (RID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
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91.2%; Score 934.5; DB 12; Length 185;
Best Local Similarity 93.4%; Pred. No. 3.5e-99;
Matches 185; Conservative 0; Mismatches 0; Indels 13;
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; Sequence 9, Application US/10083336A; Publication No. US20030181665A1; GENERAL INFORMATION:
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                                                        36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGKLTTGADVRHEIPVLPNRVGLPINQRFILV 95
2 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLFTGADVRHEIPVLPNRVGLPINQRFILV 61
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Best Local Similarity 39.5%; Pred. No. 7.6e-31;
Matches 73; Conservative 46; Mismatches 54; Indels 12; Gaps
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-356-786-10
US-08-485-286-77
US-08-488-113B-6
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US-08-646-360-6
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US-09-309-6
US-09-610-9389-6
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US-09-610-9389-6
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US-08-38-793D-61
US-09-538-793D-1
US-07-901-707-1
US-08-425-336-1
US-08-48-113B-1
US-08-48-113B-1
US-08-646-360-1
US-08-839-765-1
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US-09-610-838-1
US-09-610-838-1
US-09-610-838-1
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US-08-378-761A-27
US-08-485-286-27
                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                              328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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						ALIG	ALIGNMENTS	70				
RESULT 1 US-08-218-30 ; Sequence 1 ; Patent No.	SULT 1 -08-218-303-16 Sequence 16, A Patent No. 554	6 Appli 47867	catio	n US/	.80/	.03-16 16, Application US/08218303 5. 5547867	•					
GENER	GENERAL INFORMATION APPLICANT: Kara,	RMATION: Kara,	••	- 3	adra	, ,						
APP	APPLICANT:		•	Robert	ërt T	j.						
FILE	TITLE OF IN	INVENTION: SEQUENCES	NVENTION: SEQUENCES:	FERN 23	MEN	FERMENTATION PROCESS 23	ROCESS	'n				
S 4	CORRESPONDENCE ADDRESS ADDRESS ADDRESSEE: Cushman,	ENCE CENTRAL	ADDRESS: Cushman, Darby	55: n, De	arb	/ & Cushman	man					
on C	STREET:	Washingfor	1615 L Street,	reet,	3							
່ວນເ	STATE: I	0.0										
06	COUNTRY:	Y: U.S.A.	Α.									
O O W	拼	EADAB	LE FO	RM:								
Σ	EDIUM T	YPE:	Flop	py d	isk	-						
200	COMPUTER: OPERATING	S SYS	SYSTEM:	COMPA	atin DOS,	S-DOS	Tower 1	# # C				
CUR	CURRENT APPLICATION DATA	PLICA	TION	DATA		10.1# De		¥.				
Æ B	APPLICATION NUMBER:	NOI NOI	IUMBER	 E	3/0/	US/08/218,30	03					
40	CLASSIFICATION:	CATIC	N: 4	435								
PRI	PRIOR APPLICATION DATA:	ICATI	ON DA	TA:		, ,						
Ç [24	AFFLICATION NUMBER: US U	ATE:	26-F	EB-199	992	7,841,53	ņ					
ATT	ORNEY/A	GENT	INFOR	MATIC	ï.							
3 P4	REGISTRATION NUMBER:	TION	NUMBE	MBER: 16,773	16,	773						
PK.	REFERENCE/DOCKET NUMBER:	E/DOC	KET N	UMBE		PNK/3893/94908/MJW	3/9490	M_M_M				
TEL	TELECOMMUNICATION INFORMATION TELEPHONE: 202-861-3000	ICATI E: 2	ION INFORMAT	FORM	ATI OC	 						
1	×	20	202-822-0944	0944	,							
TOTAL	TELEX: 671	₹.		CUSH	ŕ							
SEO	SEQUENCE C	HARAC	CHARACTERISTIC	ID NO:	∓ 	 D						
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Query Match 98.4%; Score 950; DB 1; Length 267; Best Local Similarity 94.9%; Pred. No. 1.2e-102; Matches 188; Conservative 0; Mismatches 0; Indels 10; Gaps

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-218-303-16

1 MVPKQYPIINFTTAGATVQSYTNFIRAVRGRLT---

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51 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 110
                                                   61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
                                                                                                                                                 121 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISBAAR 180
                                                                                                           111 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICTQMISEAAR
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Patent No. 5376546
                                                                                                                                                                                                                                                                                                                         US-09-538-873-1
; Sequence 1, Application US/09538873
; Patent No. 6566500
; GENERAL INFORMATION:
                                                                                                                                                                                            FOYIEGEMRIRIRYNRRS 188
                                                                                                                                                                                                                                      181 FOYIEGEMRTRIRYNRRS 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 188; Conservative
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US-07-901-707-1
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                                                                51 ELSNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 110
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                        1 MVPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM PC/XY/AT Compatibles
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                          Sequence 61, Application US/08338793D
Patent No. 5840521
GENERAL INFORMATION:
APPLICANT: BATCH, Peter Thomas
TITLE OF INVENTION: VECTOR
NUMBER OF SEQUENCES: 61
CORRESPONDENCE S: 61
ADDRESSEE: INTELLECTUAL PROPERTY GROUP OF
ADDRESSEE: INTELLECTUAL PROPERTY
ADDRESSEE: INTELLECTUAL PROPERTY
ADDRESSEE: INTESURY MADISON & SUTRO, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 950; DB 2; I
Pred. No. 1.2e-102;
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TELECOMUNICATION INFORMATION:
TELECHONE: 202-861-300
TELERACOR. 202-82-0944
TELEX: 6714627 CTOT.
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/338,793D
FILING DATE: 08-No. 5840521-94
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 07/842,081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 435
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APPLICATION NUMBER: 91(
FILING DATE: 26-Feb-91
APPLICATION NUMBER: 91(
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Best Local Similarity
Matches 188; Conservat
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GENERAL INFORMATION:
APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Steve F.
APPLICANT: Carroll, Steve F.
APPLICANT: Carroll, Steve F.
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
APPLICANT: VITETIA, ELLEN S.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: BALLUNA, JOAN
APPLICANT: BALLUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
TITLE OF INVENTION: SYNDROME (VLS)
CURRENT APPLICATION NUMBER: US/09/538, 873
CURRENT PILLING DATE: 2000-03-30
EARLIER APPLICATION NUMBER: 60/126,826
EARLIER FILLING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.4%; Score 950; DB 4; Length 267; 94.9%; Pred. No. 1.2e-102; Live 0; Mismatches 0; Indels 1
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TOPOLOGY:
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APPLICANT: Better, Marc D.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 101
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                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EM PC compatible
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/901,707
FILING DATE: 19920619
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATPONNEY/AGENT INFORMATION.
                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
STREET: Wo First National Plaza, 20 South Clark
STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: NO. 537646and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE DOCKET NUMBER: 27129/30910
TELEPAN: (312) 346-5750
TELEPAN: (312) 346-5750
TELEPAN: (312) 984-5750
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Patent No. 5416202
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 YIEGEMRTRIRYNRRS 188
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                             CITY: Chicago
STATE: Illinois
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53 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 112
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Patent No. 5621083
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Studinka, Gary M.
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS: ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 267;
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                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,430
FLING DATE: 19921209
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-010-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5416202and, Greta E.
REGISTRATION NUMBER: 35302
REGISTRATION NUMBER: 35303
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                   STREET: Two First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 97.5%; Score 941; DB 1; L
Best Local Similarity 94.9%; Pred. No. 1.3e-101;
Matches 186; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 YIEGEMRTRIRYNRRS 188
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 267 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                    CITY: Chicago
STATE: Illinois
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels 10; Gaps
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Patent No. 5744580
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Setter, Marc D.
APPLICANT: Studmika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.5%; Score 941; DB 1; Length 267; 94.9%; Pred. No. 1.3e-101; tive 0; Mismatches 0; Indels
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,336
FILING DATE: 18-APR-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 PKOYPIINFTTAGATVQSYTNFIRAVRGRLT--
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 18-APR-1995
CLASSIFICATION: 530
PRICE APPLICATION DATE: 30
PRICE APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRICE APPLICATION DATE: US 07/901,707
FILING DATE: 19-JUN-1992
PRICE APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
FILING DATE: 31394
TELESTREENCE/DOCKET NUMBER: P-36,989
REPERRENCE/DOCKET NUMBER: 31394
TELESTREENCE/ATTON INFORMATION:
TELESPHONE: 312/474-6340
TELESTREENCE/ATTON INFORMATION:
TELESTREENCE/ATTON INFORMATION:
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TELESTREENCE/ATTON INFORMATION:
TELESTREENCE/ATTON INFORMATION:
TELESTREENCE/ATTON INFORMATION:
SEQUENCE CHARACTERISTICS:
TENGTH: 267 amino acids
                                                                                                                                                                                                                     PC-DOS/MS-DOS
                                                        ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MR-NY
ZURPEN: PAFFINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 YIEGEMRTRIRYNRRS 188
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amino acid
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Best Local Similarity 94.9'
Matches 186; Conservative
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                         Chicago
Illinois
Y: USA
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53 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 112
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                                                                                                                                                                                                                                                                                                                                CURENTING SYSTEM:
CURRENT APPLICATION DATA:
PELLOCATION NUMBER:
PILLING DATE:
CLASSIFICATION DATA:
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CLASSIFICATION DATA:
REPLICATION NUMBER:
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ATTORNEY AGAINT INFORMATION:
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                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08477484B
Patent No. 5756699
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 YIEGEMRTRIRYNRRS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 312/707-9155
TELEX: 650 388-1248
INPERATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 267 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
Chicago
: Illinois
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-488-113B-1
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                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGIH:
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53 SNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYTFAFGGN 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 YDRLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLFINQRFILVEL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Gaps
      Immunotoxins Comprising Ribosome-Inactivating Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 97.5%; Score 941; DB 1; Length 267; Best Local Similarity 94.9%; Pred. No. 1.3e-101; Matches 186; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11022US07/200-70.P3.C2A
                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                     ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                    CARRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,484B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR.1995
PRIOR APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY.1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DETA:
APPLICATION NUMBER:
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MONICHOLAS, Janet M. REGISTRATION NUMBER: 32,918
REGISTRATION NUMBER: 32,918
TELECOMMUNICATION: TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 YIEGEMRIRIRYNRRS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 267 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         312/707-9155
TITLE OF INVENTION: Im
TITLE OF INVENTION: Pro
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                CITY: Chicago
STATE: Illinois
                                                                                                                                                                           USA
                                                                                                                                                                                               60661
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                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-477-484B-1
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Best Local 8
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US-08-646-360-1

RESULT 9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 PKOYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILVEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 10; Gaps
Sequence 1, Application US/08646360
Patent No. 5837491
GENERAL INFORMATION:
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANdrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 941; DB 2; Length 267;
Pred. No. 1.3e-101;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
CLASSIFFICATION: DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/64,691
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRICE APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
PRICE APPLICATION NUMBER: US 07/901,707
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NUMBER: US 07/787,567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
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INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acids
TOPOLOGY: lin
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Best Local Similarity 94.9%;
Matches 186; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-646-360-1
                                                                                                                                                                                                                                                         STREET: 500 West
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
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113 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 172
                                                                        123 YDRLEQLAGNLERINIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIOMISEAARFO 182
                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09136389
Patent No. 6146850
Patent No. 6146850
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.5%; Score 941; DB 3; Length 267; 94.9%; Pred. No. 1.3e-101; cive 0; Mismatches 0; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/136,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : McAndrews, Held & Malloy, Ltd.
500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US94/05348 FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATE: US 08/064,691
FILING DATE: 09-DRC-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UIN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amir-
                                                                                                                                                               173 YIEGEMRIRIRYNRRS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 267 amino acids
amino acid
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Best Local Similarity 94.9°
Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-09-136-389-1
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STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                     US-09-136-389-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----VLPNRVGLPINQRFILVEL
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                                                                                                                                        Sequence 1, Application US/08839765
Patent No. 6146611
Patent No. 6146611
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Garry M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
TELECOMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEPAX: 50.389-1248
INFORMATION FOR SEG 1D NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/839,765
FILING DATE: 15-APR-1997
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97.5%; Score 941; DB 3; L
94.9%; Pred. No. 1.3e-101;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                  3: McAndrews, Held & Malloy, Ltd.
500 West Madison Street, 34th floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 105-APR-1997
CLASSIETCATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UNN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UNN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 10-UNN-1992
ATTORNEY APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY APPLICATION NUMBER: US 07/787,567
FILING DATE: 19-UNN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Floppy disk
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Best Local Similarity 94.94
Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-839-765-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 500 West
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC OPERATING SYSTEM:
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                                                                                                                  JS-08-839-765-1
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Gaps
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LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
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Matches 186; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                           ; MOLECULE TYPE: protein US-09-610-838-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Chicago
STATE: Illinois
COUNTRY: USA
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                                                                                                             113 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 172
                                      3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Carroll, Stephen F.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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500 West Madison Street, 34th floor
        3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT
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FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/901,707
FILING DATE: 04-NOV-1991
ATTORNEY AGENT INFORMATION:
AMAZICANISA
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FILING DATE: 13-MAY-1990
APPLICATION NUMBER: PCI/US94/05348
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APPLICATION NUMBER: US/09/136,389
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FILING DATE: 06-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 18-AUG-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                         US-09-610-838-1; Sequence 1, Application US/09610838; Patent No. 6376217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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                                                                                                                                                                                                                                                     173 YIEGEMRIRIRYNRRS 188
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INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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STATE: Illinois
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APPLICANT: Bernhard, Susan L.
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Lane, Julie A.
APPLICANT: Lei, Shau-Ping
TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                  63 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 122
                                                                                                                                                                                                                                                                                                                                                    YDRLEQLAGNLRENIELGNGPLEEAISALYYSTGGTQLPTIARSFIICIQMISBAARFQ 172
                                                                                                                                                                   62
                                                                                                        3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT-------VLPNRVGLPINQRFILVEL
                                                                                                                                                     3 PKOYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
                                                                                                                                                                                                                53 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN
                                                     0; Indels 10; Gaps
97.5%; Score 941; DB 4; Length 267; 94.9%; Pred. No. 1.3e-101; rative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Two First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION TOWNER: FCT/US92/09487
FILING DATE: 19921104
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APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UNT-1992
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-US92-09487-1; Sequence 1, Application PC/TUS9209487; GENERAL INFORMATION:
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TELECOMMUNICATION:
TELEPHONE: (312) 346-5750
TELEPAX: (312) 984-9740
                                                                                                                                                                                                                                                                                                                                                                                                                              173 YIEGEMRTRIRYNRRS 188
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                            113 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 172
                                                                                                                                                                                                                   3 PKQYPIINFITAGATVQSYINFIRAVRGRLT-----VLPNRVGLPINQRFILVEL 52
                                                                                                                                                                                                                                                        3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 62
                                                                                                                                                                            0; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08356786
Patent No. 5877305
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer WINDERTION: Marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
STREET: Exchange Place, 53 State Street
                                                                                                                                    Score 941; DB 5; Length 267;
Pred. No. 1.3e-101;
0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
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REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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94.9%;
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
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TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 8
                  LENGTH: 267 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268 amino acids
                                                                                                                              Query Match
Best Local Similarity 94.99
Matches 186; Conservative
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SEQUENCE CHARACTERISTICS
                                             ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-09487-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / MOLECULE TYPE: protein US-08-356-786-8
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RIBOSOME-INACTIVATING PROTEINS, INACTIVE
PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
USING
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                                                                                                                                                                                              53 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 112
                                                                                                                                                                                                                                                                                           113 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICLQMISEAARFQ 172
                                                                                                                                                                                                                                                                                                                                124 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 183
                                                                                                                                                                                                                                         64 SNHAELSVTLALDVTNAYVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 123
                                                                                                    ----VLPNRVGLPINQRFILVEL 52
                                                                                                                                            4 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 63
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                                                       Gaps
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                                                       10;
     97.5%; Score 941; DB 2; Length 268; 94.9%; Pred. No. 1.3e-101; ive 0; Mismatches 0; Indels 1
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                 3 PKOYPIINFTTAGATVOSYTNFIRAVRGRLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE BR
TITLE OF INVENTION: RIBOSOME-
TITLE OF INVENTION: PRECURSOR
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
                                                                                                                                                                                                                                                                                                                                                                                     173 YIEGEMRTRIRYNRRS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                     184 YIEGEMRTRIRYNRRS 199
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APPLICANT: WALSH, TERENCE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 3365
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Query Match
Best Local Similarity 94.9°
Matches 186; Conservative
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Sequence 4, Appli
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Sequence 39,
                                                                                                                                                                                                February 10, 2004, 16:26:46; Search time 24.2491 Seconds
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Seguence 6,
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Sequence 2,
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1 MVPKQYPIINFTTAGATVQS......ARFQYIEGEMRTRIRYNRRS 188
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| cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB_pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB_pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB_pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB_pep:*
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| Cgn2_6/ptcdata/1/pubpaa/US09B_PUBCOMB.pep.*
| Cgn2_6/ptcdata/1/pubpaa/US09C_PUBCOMB.pep.*
| Cgn2_6/ptcdata/1/pubpaa/US10A_PUBCOMB.pep.*
| Cgn2_6/ptcdata/1/pubpaa/US10B_PUBCOMB.pep.*
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| Cgn2_6/ptcdata/1/pubpaa/US10C_NEW_PUB.pep.*
| Cgn2_6/ptcdata/1/pubpaa/US60C_NEW_PUB.pep.*
| Cgn2_6/ptcdata/1/pubpaa/US60C_NEW_PUB.pep.*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-083-336A-4
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US-10-083-336A-3
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US-10-083-336A-3
US-10-083-336A-10
US-10-083-336A-1
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                 OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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Sequence 6, Appli Sequence 39, Appl Sequence 4, Appli Sequence 34, Appli Sequence 34, Appli	uw. v. 4 v. 9	00446 -0		Sequence 1, Appli Sequence 11, Appl Sequence 109, App Sequence 259, App Sequence 253, App
US-10-127-890-6 US-10-375-209A-39 US-10-280-679B-4 US-09-792-793A-34 US-10-375-209A-34		US-10-127-890-107 US-10-127-890-106 US-10-127-890-110 US-10-127-890-111 US-09-765-527-247 US-10-127-890-2	US-10-127-890-100 US-10-127-890-101 US-10-127-890-102 US-10-127-890-103 US-10-127-890-104 US-10-127-890-104	US-10-074-596-1 US-10-074-596-11 US-10-127-890-109 US-09-765-527-259 US-09-765-527-253
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3336 3336 305 305	297.5 297.5 273 272 2572 254	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	2242 22443 22443 23.5 243 25.5 243 25.5 25.5 25.5 25.5 25.5 25.5 25.5 25.	243.5 242.5 242.5 242.5
16 17 19 20		01 01 01 01 01 01 01 01 01 01 01 01 01 0		4 4 4 4 4 1 2 2 4 4 4 5

ALIGNMENTS

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61 TLALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 120
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                                              Sequence 8, Application US/10083336A
Publication No. US20030181665A1
GENERAL INFORMATION:
APPLICANT: Olson, Mark A
APPLICANT: Byrne, Michael P
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452USO (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
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ORGANISM: Ricinus communis
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RESULT 1
US-10-083-336A-8
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4 PKQYPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPINQRFILVELSNHAELSVTL 63
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Publication No. US20030181665A1
GENERAL INFORMATION:
APPLICANT: Olson, Mark
APPLICANT: Milard, Charles B
APPLICANT: Wannemacher, Robert W
APPLICANT: Wannemacher, Robert W
APPLICANT: Wannemacher, Robert W
APPLICANT: Wannemacher, Robert W
APPLICANT: Wannemacher, Robert W
APPLICANT: Wannemacher, Robert W
APPLICANT: Wannemacher, Robert W
APPLICANT: Wannemacher, Robert W
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT PILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                   APPLICANT: Millard, Charles B
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher, Robert W
TILLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452US0 (RIID 01-58)
FURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.1%; Score 956; DB 12; Length 188; 100.0%; Pred. No. 1.2e-101; tive 0; Mismatches 0; Indels (
                                                                                                                                     Sequence 4, Application US/10083336A Publication No. US20030181665A1 GENERAL INFORMATION:
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Matches 186; Conservative
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                      181 RIRYNRRS 188
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                                                             64 ALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGN 123
                                                                                                                                  123 LRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRI 182
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APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael B
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452US (RILD 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher, Robert W
APPLICANT: Wannemacher, Robert W
APPLICANT: Wannemacher, Robert W
APPLICANT: Wannemacher, Robert W
APPLICANT: Wannemacher, Robert W
FILLE REFERENCE: P67452USO (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
63 ALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGN
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100.0%; Pred. No. 1.2e-101;
iive 0; Mismatches 0;
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1 MVPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-
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Publication No. US20040009148A1
                   181 FQYIEGEMRTRIRYNRRS 198
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APPLICANT: GHETIE, VICTOR F.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: SMALLSHAW,
JOAN
APPLICANT: SMALLSHAW,
APPLICANT: GHETIE, VICTOR F.
APPLICANT: SMALLSHAW,
CORPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
FILE REFERENCE: UTSD:88401
CURRENT APPLICATION NUMBER: US/10/282,935
CURRENT FILING DATE: 2002-10-29
FRIOR PILING DATE: 2000-03-30
FRIOR PILING DATE: 2000-03-30
FRIOR FILING DATE: 199-03-30
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                                                                                                                                                                                      Query Match
98.4%; Score 950; DB 12; Length 198;
Best Local Similarity 94.9%; Pred. No. 6.4e-101;
Matches 188; Conservative 0; Mismatches 0; Indels 1.
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                                                                                                                                                                                                                                                                                                                                     1 MVPKQYPIINFTTAGATVQSYTNFIRAVRGRLT----
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Publication No. US20030143193A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                  TYPE: PRT ORGANISM: Ricinus communis
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                                                                                                    US-10-083-336A-7
LENGTH: 198
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APPLICANT: VITETIA, ELLEN S.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: SMALLSHAW, JOAN
APPLICANT: BALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR AMELIORATING VASCULAR LEAK
TITLE OF INVENTION: SYNROME (VLS)
FILE REFERENCE: UNSONIC: 03
CURRENT APPLICATION NUMBER: US/10/440,796
CURRENT APPLICATION NUMBER: US/09/538,873
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
NUMBER: OF SEQ ID NOS: 19
SOFTWARE: PATCHIN VET: 2.1
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Publication No. US20030181665A1
GENERAL INFORMATION:
APPLICANT: Olson, Mark A
APPLICANT: Milard, Charles B
APPLICANT: Mannemacher, Robert W
APPLICANT: Wannemacher, Robert W
APPLICANT: Robert W
APPLICANT: Robert W
APPLICANT: Robert W
APPLICANT: STORMATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 98.4%; Score 950; DB 12;
Best Local Similarity 94.9%; Pred. No. 9.8e-101;
Matches 188; Conservative 0; Mismatches 0;
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APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher, Robert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452US0 (RILD 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
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                                                  0; Indels 10; Gaps
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  Length 198;
Score 941; DB 12;
Pred. No. 6.9e-100;
0; Mismatches 0;
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  97.5%;
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                                                  186; Conservative
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Query Match
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APPLICANT: Olson, Mark A
PPLICANT: Milbard, Charles B
APPLICANT: Milbard, Michael P
APPLICANT: Wannemacher, Robert W

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53 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 112
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TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof FILE REFERENCE: P67452USO (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SRQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
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Publication No. US20030166196A1
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                    4 PKOYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILVEL
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CURRENT APPLICATION DATA:
APPLICATION UNBER: US/10/127,890
FILING DATE: 23-Apz-2002
CLASSIFICATION: <Unknown>
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ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                      97.5%; Score 941; DB 12;
94.9%; Pred. No. 7.1e-100;
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APPLICATION NUMBER: PCT/US94/05348
                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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APPLICATION NUMBER: US 08/064,691
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FILING DATE: 04-NOV-1991
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                  ORGANISM: Ricinus communis
                                                                                                                                                                                                                                                                                                                                           Matches 186; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                           US-10-083-336A-10
                                                                                                                                                                       200
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                                                                                                                                             SEQ ID NO 10
                                                                                                                                                                                                TYPE: PRT
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Sequence 2, Application US/10083336A; Publication No. US20030181665A1; GENERAL INFORMATION:
                                           173 YIEGEMRTRIRYNRRS 188
                                                                                     218 YIEGEMRTRIRYNRRS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 93.0%;
Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Ricinus communis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Ricinus communis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Olson, Mark A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 RYNRRS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 RYNRRS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-10-083-336A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISBARRFQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 PKOYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Olson, Mark A
APPLICANT: Olson, Mark A
APPLICANT: Millard, Charles B
APPLICANT: Byrne, Michael P
APPLICANT: Byrne, Michael P
TITLE OF INVENTION: Rich Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452USO (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                     Query Match 97.5%; Score 941; DB 12; Length 267; Best Local Similarity 94.9%; Pred. No. 1.1e-99; Matches 186; Conservative 0; Mismatches 0; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 941; DB 12;
Pred. No. 3.2e-99;
             NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                      ; TYPE: amino acid;
; TOPCLOGY: linear;
; MOLECULE TYPE: protein;
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-127-890-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                f Sequence 1, Application US/10083336A
f Publication No. US20030181665A1
f GENERAL INFORMATION:
                                                                                                                                                                                                                    LENGTH: 267 amino acids
ATTORNEY/AGENT INFORMATION:
                                                                                                                       TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 YIEGEMRTRIRYNRRS 188
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ORGANISM: Ricinus communis
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Best Local Similarity
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US-10-083-336A-1
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158 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 217
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                                                                                                                                                                                                                                                                                             Sequence 9, Application US/10083336A

Publication No. UG20030181665A1

GENERAL INFORMATION:

APPLICANT: Olson, Mark at A APPLICANT: Dison, Mark at APPLICANT: Byrne, Michael P

APPLICANT: Byrne, Michael P

APPLICANT: Byrne, Michael P

TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof FILE REFERENCE: P67452USO (RIID 01-58)

CURRENT APPLICATION NUMBER: US/10/083,336A

CURRENT FILING DATE: 2002-05-21

NUMBER OF SEQ ID NOS: 15
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APPLICANT: Byrne, Michael P
APPLICANT: Byrne, Michael P
APPLICANT: Wannemacher, Kobert W
TITLE OF INVENTION: Ricin Vaccine and Methods of Making and Using Thereof
FILE REFERENCE: P67452US0 (RIID 01-58)
CURRENT APPLICATION NUMBER: US/10/083,336A
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 PKQYPIINFTTAGATVQSYTNFIRAVRGRLT ---NRVGLPINQRFILVELSNHAELSVTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 96.3%; Score 929.5; DB 12; Length 185; Best Local Similarity 98.4%; Pred. No. 1.3e-98; Matches 183; Conservative 0; Mismatches 0; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 669; DB 12; Length 179; Pred. No. 1.1e-68; 0; Mismatches 0; Indels 10
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Sequence 39, Application US/09792793A

Patent No. US20020168370A1

GENERAL INFORMATION:

APPLICANT: MCMOTION:

APPLICANT: Coggins, Philip

APPLICANT: Coggins, Philip

APPLICANTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS

FILE REFERENCE: 25020-601D

CURRENT FAPILING DATE: 2001-02-22

NUMBER OF SEQ ID NOS: 93

SEQ ID NO 39

SEQ ID NO 39

LENGTH: 247
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                                                                                        53 SNHAELSVILALDVINAYVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 112
                                                                                                                  98 SNHAELSVTLALDVTNAYVVGYRAGNSAXFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 TISVAIDVINVXIMGYRAGDISYFF---NEASATEAAKYVFKDAMRKVILPYSGNYERLQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 INFITAGATVOSYTNFIRAVRGRLTVLPN------RVGLPINQRFILVELSNHAEL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 VSFRLSGATSSSYGVFISNLR---KALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 34.8%; Score 336; DB 10; Length 247;
Best Local Similarity 38.9%; Pred. No. 3.6e-30;
Matches 72; Conservative 42; Mismatches 49; Indels 22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: February 10, 2004, 16:53:54 Job time: 25.2491 secs
                                                                                                                                                                                 113 YDRLEQLAGNLRENIELGNGPL 134
                                                                                                                                                                                                                158 YDRLEQLAGNLRENIELGNGPL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Trichosanthews kirilowii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : |:
171 IGKRV 175
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US-09-792-793A-39
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OM protein - protein search, using sw model

Run on:

(without alignments) 1777.145 Million cell updates/sec February 10, 2004, 16:17:35; Search time 10.1735 Seconds

US-10-083-336A-8

1 MVPKQYPIINFTTAGATVQS......ARFQYIEGEMRTRIRYNRRS 188 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 Searched:

BLOSUM62

Scoring table:

283308 Total number of hits satisfying chosen parameters:

283308 segs, 96168682 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:* Database

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	cription	ricin D precursor	addlutinin precurs	rRNA N-qlycosidase	abrin-d precursor	abrin-c precursor	karasurin - Mongol	М	karasurin C - Tric	abrin-b precursor	abrin (clone 7.2)		beta-luffin - smoo	luffin-b - smooth	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	agglutinin I precu	rRNA N-glycosidase	rRNA N-glycosidase	mistletoe lectin I	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	antiviral protein	rRNA N-qlycosidase	betavulgin - beet	rRNA N-glycosidase	rRNA N-glycosidase
SUMMARIES		RLCSD	RLCSAG	RLTZT	532431	S16022	JU0393	JC5032	JC5606	S32430	C39761	TZLSA	\$23519	JN0108	S22494	S25560	RLPUGG	S62627	JC4840	JC4235	PD0018	JT0753	S28421	A39817	S17757	JE0401	T12573	JC4811	S28542	S28539
	DB	П	ч	Н	Ŋ	Ų	~1	71	7	7	7	7	7	7	C)	71	Н	Ŋ	N	0	7	7	C)	ď	7	7	71	N	a	7
	Length	576	564	289	528	562	247	247	289	527	251	528	278	250	277	286	286	570	245	286	254	316	294	278	313	261	289	272	253	253
ж	Query Match	7.	88.2	34.8	33.9	33.9	33.8	33.8	33.8	33.5	32.2	31.5	31.1	30.4	28.4	28.4	28.3	28.3	28.0	27.7	7.	25.2	o,	•	7.	•	•	14.3		13.2
	Score	941	851.5	336	327.5	327.5	326	326	326	323	310.5	303.5	300.5	293.5	274.5	274	273	273	270	267	\sim	43		174	17	æ	48.	138	r	127
	Result No.		2	М	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	ribosome-inactivat	rRNA N-qlycosidase	rRNA N-glycosidase	tritin - wheat	rRNA N-glycosidase	rRNA N-glycosidase	protein synthesis	rRNA N-glycosidase	hypothetical prote	shiqa-like toxin I	Shiga toxin 2 subu	Shiga toxin 2 subu	Shiga-like toxin I
S29931	805205	S28541	S46239	RLQHG2	817519	833631	A58923	RLBH	JC5848	S17932	S21940	I54695	E90779	G85640	801032
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253	283	253	310	292	293	275	253	280	280	236	319	319	319	319	318
13.2	12.8	12.7	12.6	12.5	12.1	12.0	11.9	11.8	11.6	11.4	11.3	11.2	11.2	11.2	11.1
127	124	123	122	121	116.5	116	115	114	112	110	109	108	108	108	107.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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	ricin D precursor - castor bean
	N;Contains: rRNA N-glycosidase (EC 3.2.2.2)
	C;Species: Ricinus communis (castor bean)
	C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text change 16-Jul-1999
	C; Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903
	R; Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.
	Nucleic Acids Res. 13, 8019-8033, 1985
	A, Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.
	A; Reference number: A24041; MUID:86067214; PMID:2999712
	A;Accession: A24041
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A;Molecule type: DNA A;Residues: 1-576 <HAL> A;Cross-references: GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083

Ritregear, J.W.; Roberts, L.M.
Plant Mol. Biol. 18, 515-525, 199
A;Title: The lectin gene family of Ricinus communis: cloning of a functional ricin gene & A;Reference number: S20513; MUID:92163016; PMID:1171405

S20513

A;Molecule type: DNA A;Residues: 1-576 <TRE>

Accession: A24614, MUID:8517949; NID:921084; PIDN:CAA37095.1; PID:921085 R;Lamb, F.I.; Roberts, L.M.; Lord, J.M.
Eur. J. Biochem. 148, 265-270, 1985
A;Title: Nucleotide sequence of cloned cDNA coding for preproricin.
A;Reference number: A24614; MUID:85179479; PMID:3838723

A; Molecule type: mRNA A; Residues: 12-75,'D',77-550,'R',552-576 < LAM> A; Residues: 12-75,'D',77-550,'R',552-576 < LAM> A; Cross-references: GB:X02388; NID:g21077; PIDN:CAA26230.1; PID:g21078 A; VSshitake, S.; Funatsu, G.; Punatsu, M. Agric. Biol. Chem. 42, 1267-1274, 1978 A; Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile charactering number: A03372

A; Accession: A03372

A; Molecule type: protein A; Residues: 36-97, '0', 99-109, 'S',111-269, 'D',272-283,'L',285-288,290-302 <YOS> A; Residues: 36-97, '0', 99-109, 'S',111-269, 'D',272-283,'L',285-288,290-302 <YOS> A; Note: this paper cites the others in the series providing experimental details for the R; Araki, T.; Funatsu, G. FEBS Lett. 191, 121-124, 1985 FEBS Lett. 191, 121-124, 1985 A; Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptophan A; Reference number: A24010

A; Accession: A24010

A; Molecule type: protein A; Residues: 315-383, 'PS', 386-576 <ARA>

R;Funatsu, G.; Kimura, M.; Funatsu, M. Agric. Biol. Chem. 43, 2221-2224, 1979 A;Title: Primary structure of Ala chain of ricin D.

A; Reference number: A03374

A;Accession: A03374 A;Molecule type: protein

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                                                                                                                                                                                                                                               A/Contents: annotation; active site
A/Contents: annotation; active site
R/Ritcheric annotation; active site
R/Ritcheric annotation; active site
Proceins 10, 26-269, 1991
A/Title: Structure of ricin B-chain at 2.5 angstrom resolution.
A/Ritcheric contents: annotation; X-ray crystallography, 2.5 angstroms
R/Ritcheric annotation; X-ray crystallography, 2.5 angstroms
R/Ratin, B.J.; Collins E.J.; Robertus, J.D.
R/Ritcheric annotation; X-ray crystallography, 2.5 angstroms
R/Ratin, B.J.; Collins E.J.; Robertus, J.D.
R/Ritcheric annotation; X-ray crystallography, 2.5 angstroms
R/Ratin, B.J.; Collins E.J.; Robertus, J.D.
R/Rotchers: annotation; X-ray crystallography, 2.5 angstroms
C/Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which
C/Comment: The A chain inhibits protein synthesis; it inactivates the 60S ribosomal subunto the cell of the A chain; B chains are also responsible for cell agglutination (lecting Cycomment: This protein is cytotoxic and very poisonous to animals.
C/Comment: This protein is cytotoxic and very poisonous to animals.
C/Comment: This protein is cytotoxic and very poisonous to animals.
C/Comment: This protein is cytotoxic and very poisonous to animals.
C/Comment: This protein is cytotoxic and very poisonous to animals.
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C/Comment: This protein is cytotoxic and very poisonous to animals.
C/Comment: This protein is cytotoxic and very poisonous to animals.
C/Comment: This protein is cytotoxic and very poisonous to animals.
C/Comment: This protein is cytotoxic and well a #status experimental A #status experimental and the animal and the animal animals.
C/Comment: S/CAPCADOUCT: ricin D chain B #status experimental
R/115,132/Active site: Alf #status experimental
R/115,132/Active site: Alf #status experimental
R/115,132/Active site: Alf #status experimental
R/115,132/Active site: Alf #status experimental
R/124,333,337-334,455-478,504-531
R;Ready, M.P.; Kim, Y.; Robertus, J.D.
Proteins 10, 270-278, 1991
Proteins 10, 270-278, 1991
A;Title: Shie-directed mutagenesis of ricin A-chain and implications for the mechanism A;Reference number: A48237; MUID:91352006; PMID:1881883
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Nicontains: FRNA N-glycosidase (EGS 3.2.2.22)
C.Species: Ricinus communis (castor bean)
C.Species: Ricinus communis (castor bean)
C.Species: N-coresion: A24261; A24210
R.Roberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.
J. Biol. Chem. 260, 15682-15686, 1985
A.Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin. A, Reference number: A24261; MUID:86059449; PMID:2999130
A, Accession: A24261
A, Molecule type: MRNA
A, Residues: 1-564 < ROB>
A, Cross-references: GB:MI2089; NID:gl69700; PIDN:AAA33869.1; PID:gl69701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 YDRLEQLAGNIRENIELGNGPLEBAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKQYPIINFTTAGATVQSYTNFIRAVRGRLT----
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Best Local S
Matches 186
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A,Molecule type: protein
A;Residues: 303-325, F',327-330, T',332-361, D',363-373, G',375-403, T',405-551, V',553-
C;Comment: This protein has strong agglutinating activity and weak cytotoxicity compared
C;Superfamily: ricin; rRNA N-glycosidase homology
C;Reywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
F;12-240 bomain: signal sequence #status predicted <STG>
F;25-290/Product: agglutinin chain A #status predicted <ACH>
F;35-281/Domain: rRNA N-glycosidase homology <RNG>
F;319-361,365-465-443,489-528,531-564/Region: 40-residue repeats
F;319-361,365-465-443,489-528,531-564/Region: 40-residue repeats
F;319-361,365-382-364,489-528,531-564/Region: Ann #status predicted
F;104,147,231,232/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;282-306,322-341,365-382-453-466,492-509/Disulfide bonds: #status predicted
F;324,337,348/Binding site: N-acetylgalactosamine (Asp, Glu, Ann) #status predicted
F;356,557/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
F;356,557/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
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A,Residues: 1-289 <SRN>
A,Cross-references: GB-M34858; NID:g170536; PIDN:AAA34207.1; PID:g170537
A,Experimental source: tuber
R;Chow, T.P.; Feldman, R.A.; Lovett, M.; Piatak, M.
J. Biol. Chem. 265, 8670-8674, 1990
A,Title: Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I rib
A,Reference number: A36274; MUID:90256790; PMID:2341400
R;Araki, T.; Yoshioka, Y.; Funatsu, G.
Biochim. Blophyr. Acta 872, 277-285, 1986
A;Title: The complete amino acid sequence of the B-chain of the Ricinus communis aggluti:
A;Reference number: A24210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 SNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 112
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A; Residues: 1-233, Tr, 235-246, 'M', 248-289 < CHO>
A; Cross-references: GB: J05434; NID: g170534; PIDN: AAA34206.1; PID: g170535
B; Zheng, H.G.; Mang, B.; Shao, P.Z.; Yang, X.R.
Acta Genet. Sin. 21, 42-51, 1994
A; Title: Cloning and DNA sequencing of the gene encoding Trichosanthin.
A; Reference number: JC1093; MUID: 94271613; PMID: 8003348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
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Pred. No. 2.9e-70;
7; Mismatches 8; Indels 11.
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A; Molecule type: protein

A; Accession: JT0003

A; Accession: A36273

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Alloss letterwises desiros of an A chain, which inhibits protein synthesis by inactivating the A and B chains are linked by a single disulfide bond, which is essential for toxicit (c) superfamily: rich; rRNA N-glycosidase homology (c) Keywords: disulfide bond; duplication; glycosidase; hydrolase; hydrolase; lectin; py F;1-251/Product: abrin-d chain A #status predicted «ACH»
F;7-251/Product: abrin-d chain B #status predicted «BCH»
F;261-258/Product: abrin-didone carboxylic acid (GIn) #status predicted
F;164,167/Active site: Glu, Arg #status predicted
F;164,167/Active site: Glu, Arg #status predicted
F;260,253,354,401,402/Binding site: Carbohydrate (Asp, Asn) #status predicted
F;280,312/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
F;500,521/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
                                                                                                                                                                                                                                 three distinct isoabrins determined by cDNA sequencing. Cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and the expression of the A-chair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X55667; NID:g16084; PIDN:CAA39202.1; PID:g16085
C;Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating
The A and B chains are linked by a single disulfide bond, which is essential for toxicit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 ELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 RESIEVGIDVINAYVVAYRAGSQSYFL---RDAPASASTYLFPGTQ-RYSLRFDGSYGDL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 EQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 QYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVELSNHA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997 C;Accession: S32431; S34408 R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y. J. Mol. Biol. 229, 263-267, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
C;Species: Abrus precatorius (Indian licorice)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68; Indels
                                                                                                                                                                                                                                                              A; Reference number: S32429; MUID: 93132798; PMID: 8421313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R,Wood, K.A.; Lord, J.M.; Wawrzynczak, E.J.; Piatak, M. Bur. J. Biochem. 198, 723-732, 1991
A;Title: Preproabrin: genomic cloning, characterisation
A;Reference number: S16022; MJID:91266957; PMID:2050149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.9%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ,171-320,'L',322-528 <HU2>
                                                                                                                                                                                                                                                                                                                                                                                                                   A.Cross-references: GB:M98346
R;Hung, C.; Lee, M.; Lee, T.; Lin, J.
submitted to the EMBL Data Library, March 1993
                             C;Species: Abrus precatorius (Indian licorice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  precursor - Indian licorice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82; Conservative
                                                                                                                                                                                                                        A, Title: Primary structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB: M98346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: $34408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 EMRTRIR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 RVGVSIR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-528 <HUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-562 < WOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-169,'C'
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                                                                                                                                                                                                                                                                                                             A; Accession: S32431
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A; Molecule type: DNA
A; Residues: 1-72, 'V', 74-90, 'S', 92-233, 'T', 235-267, 'D', 269-289 <ZHE>
A; Residues: 1-72, 'V', 74-90, 'S', 92-233, 'T', 235-267, 'D', 269-289 <ZHE>
A; Cross-references: GB:S70176; NID:g547148; PIDN:AAB31048.1; PID:g547149
R; Collins, E.J.; Robertus, J.D.; Lopresti, M.; Stone, K.L.; Williams, K.R.; Wu, P.; Hwan J. Biol. Chem. 265, 8665-8669, 1990
A; Title: Primary amino acid sequence of alpha-trichosanthin and molecular models for abz A; Reference number: A36273; MUID:90256789; PMID:2341399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-27 R;Xiong, J.P.; Xia, Z.X.; Wang, Y. Nat. Struct. Biol. 1, 695-700, 1994
A;Title: Crystal structure of trichosanthin-NADPH complex at 1.7 Angstroms resolution re A;Reference number: A58622; MUID:95360714; PMID:7634073
                                                                                                                                                                                                                                                                                                                              A,Molecule type: protein
A,Residues: 24-270 <CCL>
KWang, Y.; Qian, R.Q.; Gu, Z.W.; Jin, S.W.; Zhang, L.Q.; Xia, Z.X.; Tian, G.Y.; Ni, C.Z
Pure Appl. Chem. 58, 789-798, 1986
A,Title: Scientific evaluation of Tian Hua Fen (THF): history, chemistry and application
A,Reference number: JT0003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Residues: 24-56, 11,58-59, 11,61-71,11,73-81,85-86,15,88-92, DAGLPRNAVL,93-142,6L/A.Experimental source: tuber
A.Experimental source: tuber
A.Experimental source: tuber
Sthuang, 0.; iu., S.; Tang, Y.; Jin, S.; Wang, Y.
Submitted to the Brookhaven Protein Data Bank, July 1994
A.Reference number: A67091; PDB:1MRJ
A.Reference number: A67091; PDB:1MRJ
A.Reference number: A67091; PDB:1MRJ
B.Huang, 0.; iu., S.; Tang, Y.; Jin, S.; Wang, Y.
Submitted to the Brookhaven Protein Data Bank, July 1994
A.Reference number: A67092; PDB:1MRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with formycin, residues 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 SVILALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----RVGLPINQRFILVELSNHAEL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 VSFRLSGATSSSYGVFISNLR---KALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADE 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Contents: annotation; X-ray crystallography, 1.7 angstroms C; Comment: Alpha-trichosanthin has been used to induce abortions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 289;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Contents: annotation; X-ray crystallography, 1.6 angstroms, R;Xiong, J.T.; Xia, Z.Y.; Wang, Y. submitted to the Brookhaven Protein Data Bank, December 1994 A; Reference number: A66711; PDB:1TCS
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34.8%; Score 336; DB 1; 38.9%; Pred. No. 2.6e-23; 42; Mismatches

9 INFTTAGATVQSYTNFIRAVRGRLTVLPN----

72; Conservative

Best Local Similarity

Matches

ð

ö

Query Match

C;Genetics:

s32431
abrin-d precursor - Indian licorice (fragment)
N;Contains: rRNA N-glycosidase (EC 3.2.2.2) RESULT 4

MRTRI 182

178

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a

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ĸa.

Length 247;

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A;Residues: I-247 <KON>
C;Comment: This protein belongs to type I ribosomal-inactivating proteins which catalytic
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;4-243/Domain: rRNA N-glycosidase homology <RNG>
                                                                                                                                                                                                                 R;Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.
Biol. Pharm: Bull. 19, 1488-1489, 1996
Biol. A;Fille: Amino acid sequences and ribosome-inactivating activities of karasurin-B and
A;Reference number: UC5032; MUID:97108848; PMID:8951169
                                                                                                                          C;Species: Trichosanthes Kirilowii var. japonica
C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 23-May-1997

    Trichosanthes kirilowii var. japonica

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.8%;
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Best Local Similarity 39.64
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                      A,Accession: JC5032
A,Status: preliminary
A,Molecule type: protein
A,Residues: 1-247 <KON>
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Best Local Similarity
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A; Status: preliminary
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                                                                                                                                                                                      C; Accession: JC5032
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                                                                                                        karasurin-B
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C;Superfamily: ricin; rRNA N-glycosidase homology
C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglutamic acid
F;35-28PFroduct: abrin-c chain A #status predicted ACH>
F;41-280/Domain: rRNA N-glycosidase homology ~RNG>
F;295-562/Product: abrin-c chain B #status predicted ACH>
F;295-562/Product: abrin-c chain B #status predicted ACH>
F;295-562/Product: abrin-c chain B #status predicted ACH>
F;295-562/Product: abrin-c chain B #status predicted ACH>
F;295-262/Product: abrin-c chain B #status predicted ACH
F;211-280;300/Binding site: substrate (TYr, Tyr, Glu, Asn) #status predicted
F;108,147,229,230/Binding site: exbohydrate (Asn) (covalent) #status predicted
F;234,287,395,435,436,Binding site: arbohydrate (Asn) (covalent) #status predicted
F;221,346/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
F;324,555/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Trichosanthes Kirilowii (Mongolian snake-gourd)
C;Species: Trichosanthes Kirilowii (Mongolian snake-gourd)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 12-Apr-1995
C;Accession: U0393; PS0163
R;Toyokawa, S.; Takeda, T.; Kato, Y.; Wakabayashi, K.; Ogihara, Y.
Chem. Pharm. Bull. 39, 1244-1249, 1991
A;Title: The complete amino acid sequence of an abortifacient protein, karasurin.
A;Reference number: U0393; MUID:92005921; PMID:1914000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 RESIEVGIDVTNAYVAYRAGSQSYFL---RDAPASASTYLFPGTQ-RYSLRFDGSYGDL 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 EQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIOMISEAARFQYIEGEMRT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 LALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFIDVQNRYTFAFGGNYDRLEQLA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 ELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYIFAFGGNYDRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 1-247 <TOY2.
A;Residues: 1-247 <TOY2.
A;Note: a sequence which lacks Ala-247 is also shown in this publication C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C;Keywords: abortifaciant
F;4-243/Domain: rRNA N-glycosidase homology <
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.8%; Score 326; DB 2; Length 247; 39.6%; Pred. No. 1.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                           33.9%; Score 327.5; DB 2
43.9%; Pred. No. 3.6e-22;
tive 22; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4-243/Domain: rRNA N-glycosidase homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             karasurin - Mongolian snake-gourd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 39.00.
-20 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 EMRTRIR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 RVGVSIR 214
                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity
Matches 82; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 RV 175
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karasurin C - Trichosanthes kirilowii var. japonica
%Contains: karasurin A
%Contains: karasurin A
%Contains: karasurin A
%Contains: karasurin A
%Contains: karasurin A
%Contains: Trichosanthes kirilowii var. japonica
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 19-Jul-2002
%Accession: JGS605, JGS033
R;Mizukami, H.; Iida, K.; Kondo, T.; Ogihara, Y.
Biol. Pharm. Bull. 20, 711-713, 1997
Biol. Pharm. Bull. 20, 711-713, 1997
A;Title: Cloning and bacterial expression of a gene encoding ribosome-inactivating prote A;Accession: JGS606, MUID:97356562; PMID:9212998
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A,Molecule type: protein

B,Residues: 22-270 excons

C,Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, aborti

C,Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, aborti

C,Comment: This protein belongs to type I ribosomal-inactivating proteins which catalyti

C,Superfamily: rRNA N-glycosidase, rRNA N-glycosidase homology

E,22-270/Product: karasurin C #status predicted eMAC>

F,24-270/Product: karasurin A #status predicted eMAA>

F,24-270/Product: rRNA N-glycosidase homology eRNG>
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A; Residues: 1-289 cALIZ.
A; Residues: 1-289 cALIZ.
A; Cross-references: DDBJ:AB000666; NID:q2329830; PIDN:BAA21786.1; PID:g2329831
R; Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.
R; Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.
Biol. Pharm: Bull. 19, 1465-1488, 1996
A; Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and ka
A; Reference number: JC5032; MUID:97108848; PMID:8951169
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                                                                                                                                                                        9 INFTTAGATVQSYTNFIRAVR-----GRLTVLP-NRVGLPINQRFILVELSNHAELSVT
                                                                                                                                                                                                                               2 VSFRLSGATSSSYGVFISNLRKALPYERKLYDIPLLRSTLPGSQRYALIHLTNYADETIS
                                                                                                                                                                                                                                                                                                                                                      62 LALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLEQLA
                                                                                      16; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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39.6%; Pred. No. 2.1e-22;
live 44; Mismatches 50; Indels 16;
                                                                                      50; Indels
; Score 326; DB 2;
; Pred. No. 1.7e-22;
44; Mismatches 50
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A;Title: Primary structure of three distinct isoabrins determined by cDNA sequencing. Cor A;Reference number: S32429; MUID:93132798; PMID:8421313
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R;Evensen, G.; Mathiesen, A.; Sundan, A.
N. Biol. Chem. 266, 6848-6852, 1991
A;Hitle: Direct molecular cloning and expression of two distinct abrin A-chains.
A;Reference number: A39761; MUID:91201329; PMID:2016300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Cross-references: EMBL:X54872; NID:g16088; PIDN:CAA38654.1; PID:g16089
C;Superfamily: ricin; rRNA N-glycosidase homology
C;Superfamily: ricin; rRNA N-glycosidase; hydrolase; lectin; toxin
F:1-251/Product: abrin (clone 7.2) chain A #status predicted <ACH>
F;7-246/Domain: rRNA N-glycosidase homology <RNG>
F;7-246/Domain: rRNA N-glycosidase homology <RNG>
F;74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;164,167/Active site: Glu, Arg #status predicted
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C;Species: Abrus precatorius (Indian licorice)
C;Date: 21-Feb-1992 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N; Contains: rRNA N-glycosidase (EC 3.2.2.22)
C; Species: Abrus precatorius (Indian licorice)
C; Species: Abrus precatorius (Indian licorice)
C; Species: Abrus precatorius (Indian licorice)
C; Species: 3D-6-1993 #sequence revision 01-Aug-1997 #text change 16-Jul-1999
C; Accession: S32429; JT0202; A39761; JC1398; S14472; S24133; S74110; S74111
R; Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: DNA
A;Residues: 1-251 <FVE>
R;Revensen, G.; Mathiesen, A.; Sundan, A.
Submitted to the EMBL Data Library, October 1990
A;Description: Direct molecular cloning of two distinct abrin A-chains.
A;Reference number: S14471
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                                                                                                                                                                   Indian licorice (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.2%; Score 310.5; DB 2 43.2%; Pred. No. 4.7e-21; rative 22; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TZLSA
abrin-a precursor - Indian licorice (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: nucleic acid sequence not shown
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A; Residues: 'M', 1-251 <EV2>
                                                                                                                                                                   abrin (clone 7.2) precursor
173 RVGVSIRTN 181
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A; Residues: 'E', 2-528 <HUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
----- 79; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 RIR 183
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A; Rolecule type: protein
A; Rolecule type: protein
A; Residues: 260-281, 'D', 283-290, 'N', 292-349, 'PQ', 352-377, 'N', 379-425, 'M', 427, 'D', 429-430
A; Residues: 260-281, 'D', 283-290, 'N', 292-349, 'PQ', 352-377, 'N', 379-425, 'M', 427, 'D', 429-430
C; Superfamily: ricin; rRNA N-glycosidase homology
C; Reywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; pr F; 7-245/Domain: rRNA N-glycosidase homology < RNGP.
F; 7-245/Domain: rRNA N-glycosidase homology < RNGP.
F; 7-245/Domain: rRNA N-glycosidase homology < RNGP.
F; 7-245/Domain: rRNA N-glycosidase homology < RNGP.
F; 7-245/Domain: rRNA N-glycosidase homology < RNGP.
F; 7-245/Domain: rRNA N-glycosidase homology < RNGP.
F; 7-245/Domain: rRNA N-glycosidase homology < RNGP.
F; 7-245/Domain: rRNA N-glycosidase homology < RNGP.
F; 7-245/Domain: rRNA N-glycosidase homology < RNA N-glycosidase; lectin; predicted F; 74,113,194,195/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted F; 153,166/Active site: Glu, Arg #status predicted F; 269,455,416-429,455-472/Disulfide bonds: #status predicted F; 287,311/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted F; 499,520/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A)Residues: 1-527 cHUN>
A)Cross-references: GB:M98345; NID:g166296; PIDN:AAA32625.1; PID:g166297
A)Cross-references: GB:M98345; NID:g166296; PIDN:AAA32625.1; PID:g166297
B;Kimura, M.; Sumizawa, T.; Fundsu. T.; Pidnatsu, G
Biosci. Biotechnol. Biochem. 57, 166-169, 1993
A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic A;Reference number: JC1398; MUID:93169023; PMID:7763422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Contains: rRNA N-glycosidase (BC 3.2.2.2)
C;Species: Abrus precatorius (Indian licorice)
C;Species: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 20-Aug-1999
C;Accession: S32430; JC1399
C;Accession: S32430; JC1399
R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
A;Title: Primary structure of three distinct isoabrins determined by cDNA sequencing.
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                                                                                                                                                                                                                                                                                        GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 180
                                                                                                                                                                                                                                                                                                                               LALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFIDVQNRYIFAFGGNYDRLEQLA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 ELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TESIEAGIDVSNAYVVAYRAGNRSYFL---RDAPTSASRYLFTGTQ-QYSLRFNGSYIDL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQLAGNIRENIELGNGPLEEALSALYYYSTGGTQLPTLARSFILCIQMISEAARFQYIEG 176
                                                            --GRLTVLP-NRVGLPINORFILVELSNHAELSVT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----VLPNRVGLPINQRFILVELSNHA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ODQVIKETIBGATSOSYKOFIBALRORLIGGLIHGIPVLPDPTTLOBRNRYISVELSNSD 60
                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: S32429; MUID: 93132798; PMID: 8421313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               abrin-b precursor - Indian licorice (fragment)
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                     INFITAGATVOSYTNFIRAVR-
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                                                                                                                                                                                                                                                                                                                                                                                                                            181 RI 182
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Best Local
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RESULT 12
S23519
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C.Comment: Abrin-a is more toxic than ricin. The toxin consists of an A chain, which inh
C.Comment: Abrin-a is more toxic than ricin. The toxin consists of an A chain, which inh
C.Comment: Abrin-a is more toxic than ricin. The A and B chains are linked by a single disulfil
C.Superfamily: ricin, rRNA N-glycosidase homology
C.Keywords: duplication; glycoprotein; glycosidase, hydrolase; lectin; pyroglutamic acid
F.1-251/Product: abrin-a chain A #status experimental <ACH>
F.1-251/Product: abrin-a chain B #status experimental <ACH>
F.261-528/Product: abrin-a chain B #status experimental <ACH>
F.261-528/Product: abrin-a chain B #status experimental <ACH>
F.261-528/Product: abrin-a chain B #status experimental
F.261-528/Product: abrin-a chain B #status predicted
F.261-528/Product: abrin-a chain B #status predicted
F.261-528/Product: abrin-a chain B #status predicted
F.261-528/Product: abrin-a chain B #status predicted
F.261-528/Product: abrin-a chain B #status predicted
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F.261-528/Product: abrin-a chain B #status predicted
F.261-528/Product: abrin-a chain B #status predicted
F.261-528/Product: abrin-a chain B #status predicted
F.261-261-268/Product: abrin-a chain B #status predicted
F.261-261-261/Painding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Kimura, M.; Sumizawa, T.; Funatsu, G.
Bisoci. Biotechnol. Biochem. 57, 166-169, 1993
A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic
A;Reference number: JC1398; MJID:93169023; PMID:7763422
        amino acid sequence of the A-chain of abrin-a, a toxic protein frd
                                                                                                                         A;Molecule type: protein
A;Residues: 1-201,203-251 <FUN>
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
                                                                                                                                                                                                                                         RiEvensen, G.; Mathiesen, A.; Sundan, A. Datol. Chem. 266, 6848-6852, 1991
A;Title: Direct molecular cloning and expression of two distinct abrin A-chains. A;Reference number: A39761; MUID:91201329; PMID:2016300
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A; Residues: 262-297, Y', 299-426, 'L', 428-466, 'P', 468-482, 'L', 484-528 < CHE>
A; Residues: 262-297, Y', 299-426, 'L', iniaw, Y.C.; Chen, J.K.; Lin, J.Y.
R:Lin, S.H.; Chow, L.P.; Chen, Y.L.; Liaw, Y.C.; Chen, J.K.; Lin, J.Y.
Eur. J. Biochem. 240, 564-569, 1996
A; Title: Probing the domain structure of abrin-a by tryptic digestion.
A; Reference number: S74110; MUID:97008945; PMID:8856055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 'ME', 2-251 <EV2>
A;Cross-references: EMBL:X54873; NID:g16090; PIDN:CAA38655.1; PID:g16091
R;Chen, Y.L.; Chow, L.P.; Tsugita, A.; Lin, J.Y.
FEBS Lett. 309, 115-118, 1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Evensen, G.; Mathiesen, A.; Sundan, A. submitted to the EMBL Data Library, October 1990
A;Description: Direct molecular cloning of two distinct abrin A-chains.
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A;Residues: 261-347,'T',349-351,'A',353-357,'L',359-528 <KIM>
A;Experimental source: seed
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A,Residues: 262-276,'X',278-280,329-348;369-388;399-418 <LIW>
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A; Residues: 89-108;154-172 <LIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB:X54872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ,2-251 <EVE>
A; Title: The complete amind A; Reference number: JT0202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
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Best Local Simi:
Matches 76;
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Gaps

64; Indels 19;

; Pred. No. 5.3e-20; 26; Mismatches 64.

41.18;

Similarity

Conservative

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beta-luffin, another ribosome-inactivating
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C;Species: Luffa cylindrica (smooth loofah)
C;Date: 0.4-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 07-May-1999
C;Accession: JN0108
R;Islam, M.R.; Hirayama, H.; Funatsu, G.
R;Islam, M.R.; Hirayama, H.; Funatsu, G.
A;Title: Complete amino add sequence of luffin-b, a ribosome-inactivating protein from A;Reference number: JN0108; MUID:91248488; PMID:1368666
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                                                                                                                                                                                                                                                                                              119 WAHQSRQQIPLGLQALTHGIS---FFRSGGNDNEEKARTLIVIIQMVAEAARFRYISNRV 175
                                                                                                                       61 TLALDVINAYVVGYRAGNSAYFFH--PDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 118
                                                                                                                                                                                 65 EVGIDVTNAYVVAYRAGTQSYFLRDAPSSASD----YLFTGT-DQHSLPFYGTYGDLER 118
                                                                                                                                                                                                                                                     .19 LAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 LAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 VSFSLSGADSKSYSKFITALRKALPSKEKVSNIPLLIPSASGA---SRYILMQLSNYDAK 80
   9
                                                                64
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C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Aug-1999
C;Accession: 823119; 823113
R;Kataoka, J; Habuka, N; Miyano, M; Masuta, C; Koiwai, A.
R;Kataoka, Di; Habuka, N; Miyano, M; Masuta, C; Koiwai, A.
R;Tatt Mol. Biol. 19, 887-889, 1992
A;Title: Nucleotide sequence of cDNA encoding beta-luffin, another ribosome-A;Reference number: 823519; MUID:92353400; PMID:1643290
                                     59 SVTLALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFIDVQNRYTFAFGGNYDRLEQ
----TVLPNRVGLPINQRFILVELSNHAELSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --TVLPNRVGLPINQRFILVELSNHAEL
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C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;26-264/Domain: rRNA N-glycosidase homology <RNG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.1%; Score 300.5; DB 2; 35.3%; Pred. No. 4.4e-20; ive 43; Mismatches 57;
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9 INFTTAGATVOSYTNFIRAVRGRL--
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Matches	OY :
RESULT 14 S22494 TRNA N-glycosidase (EC 3.2.2.2) alpha-luffin precursor - smooth loofah N.Alternate names: protein synthesis inhibitor; ribosome-inactivating protein luffin-A C;Decies: Luffa cylindrica (smooth loofah) C;Decies: Luffa cylindrica (smooth loofah) C;Decies: Luffa cylindrica (smooth loofah) C;Decies: Luffa cylindrica (smooth loofah) C;Decies: Luffa cylindrica (smooth loofah) C;Decies: Luffa cylindrica (smooth loofah) C;Decies: Luffa cylindrica (smooth loofah) C;Decies: Luffa cylindrica (smooth loofah) C;Decies: Luffa cylindrica (smooth loofah) C;Decies: Luffa cylindrica (smooth loofah) C;Decies: Luffa cylindrica (smooth loofah) C;Decies: Lipsubka, N.; Miyano, M.; Masuta, C.; Koiwai, A. A;Teference number: S22494; MUD:92288316; PMD:1600156 A;Accession: S22494 A;Molecule type: mRNA A;Residues: L-277 cKAT-> A;Cross-reference: EMBL:X62371; NID:919145; PIDN:CAA44229.1; PID:91946 A;Title: Complete anina acid sequence of luffin-a, a ribosome-inactivating protein from A;Accession: S26390; MUID:91248471; PMID:1368651	RESULT 15 525560 C;Date: 22-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 20-Aug-1999 C;Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 20-Aug-1999 C;Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 20-Aug-1999 C;Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 20-Aug-1999 R;Ortigao, M.; Better, M. Nucleic Acids Res. 20, 4662, 1992 A;Title: Momordin II, a ribosome inactivating protein from Momordica balsamina, is homolc A;Feference number: 825560; MUID:93027170; PMID:1408771 A;Recession: 825560 A;Status: preliminary A;Status: preliminary A;Status: preliminary A;Status: preliminary A;Status: preliminary A;Status: preliminary C;Reywords: 1286 cogr. C;Reywords: glycosidase; rRNA N-glycosidase homology C;Reywords: glycosidase; rRNA N-glycosidase homology cogr. C;Reywords: glycosidase; rRNA N-glycosidase homology C;Reywords: glycosidase; rRNA N-glycosidase homology C;Reywords: glycosidase; rRNA N-glycosidase homology C;Reywords: glycosidase; rRNA N-glycosidase homology C;Reywords: glycosidase; rRNA N-glycosidase homology C;Reywords: glycosidase; rRNA N-glycosidase homology C;Reywords: glycosidase; rRNA N-glycosidase homology C;Reywords: glycosidase; rRNA N-glycosidase homology C;Reywords: glycosidase; rRNA N-glycosidase homology C;Reywords: glycosidase; rRNA N-glycosidase; rRNA N-gly
A, Moclecule type: procein A, Residues: 21-53, 11',55',1',57-86',SQL',90-154,'L',156-157,'I',159-173,'L',175-209,'SL' A; Islaum, M.R.; Mishida, H.; Funatsu, G. A; Fitle: Complete amino acid sequence of luffin-a, a ribosome-inactivating protein from A; Recence number: J183-1345, 1990 A; Fitle: Complete amino acid sequence of luffin-a, a ribosome-inactivating protein from A; Accession: J40202; MUID: 91197482; PMID: 1368623 A; Recence number: J70202; MUID: 91197482; PMID: 1368623 A; Readata: Sprotein A; Recence number: Second J7, S5', I', S7-86', SQL', 90-154', L', 156-157', I', 159-173', L', 175-209,'SL' A; Ramakrishnan, S.; Enghlid, J.J.; Bryant Jr., H.L.; Xu, F.J. A; Ramakrishnan, S.; Enghlid, J.J.; Bryant Jr., H.L.; Xu, F.J. A; Reference number: A32542; MUID: 89246493; PMID: 2719679 A; Reference number: A32542; MUID: 89246493; PMID: 2719679	2 VPKQYPIINFTTAGATVQSYTNFIRANRGGLTVLPHRVGLP1NORFILVELSN 54

Search completed: February 10, 2004, 16:28:02 Job time : 10.1735 secs

A; Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA ther C; Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C; Superfamily: rRNA N-glycosidase; hydrolase; seed; toxin
F; 1-20/Domain: signal sequence #status predicted <SIG>
F; 21-26/Product: rRNA N-glycosidase alpha-luffin #status experimental <MAT>
F; 24-26/Domain: rRNA N-glycosidase homology <RNG>
F; 268-27/Domain: rRNA N-glycosidase homology <RNG>
F; 268-27/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F; 28, 25, 246/Binding site: carboxyl-terminal carboxyl-terminal propeptide #status predicted <CTP>
F; 290, 179, 182/Active site: Tyr, Glu, Arg #status predicted

A;Status: preliminary A;Molecule type: protein A;Residues: 21-28,'G',30,'X',32-34,'K',36-40 <RAM> C;Function:

/ Match 28.4%; Score 274.5; DB 2; Length 277; Local Similarity 33.3%; Pred. No. 1.1e-17; nes 63; Conservative 42; Mismatches 61; Indels 23; Gaps

Query Match Best Loca Matches us-10-083-336a-8.rsp

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GenCore version 5.1.6
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OM protein - protein search, using sw model

February 10, 2004, 16:13:55; Search time 6.27131 Seconds (without alignments) 1409.756 Million cell updates/sec Run on:

US-10-083-336A-8 965 1 MVPKQYPIINFTTAGATVQS.....ARFQYIEGEMRTRIRYNRRS 188 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 segs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

127863

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

κο	Description			Н	trichosa		tricho				bryonia	abrus p	luffa	cucumi	luffa C	momor		viscum alb		P33186 delonium mu				phytolacc						dianthus c	hordeum v	P27560 saponaria o			
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RIPX MAIZE	SLTA_BPH19	RIP9 MAIZE	SLTA_BPH30	SYV AQUAE	Y348 MYCPN	J160 HORVU	ORPB_HUMAN	HAPT VIBCH	RIP4 SAPOF	NPRV_VIBPR	GPH_HAEIN	
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10.3	10.0	6.6	6.6	8.9	8.4	8.2	8.1	7.9	7.9	7.8	7.8	
66	96.5	95.5	95.5	85.5	81.5	79	78	76.5	92	75.5	75	
34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

CI_RICCO _RICI_RICCO STA _P02879; P02880;		DE Ricin precursor [Contains: Ricin A chain (rRNA N-glycosidase)		tophyta, Embryophyta, Tracheor			RP SEDIENCE FROM N.A.		Halling	ka weaver K.F.; RT "Genomic cloning and characterization of a ricin gene from Diginis	communis.";				Tregear J.W., Roberts L.M.;	"ine lectin gene family of Ricinus communis: cloning of a ricin gene and three lectin nashdoganss ".				Lamb A., Roberts L.M., Lord J.M.;	"Nucleotide Bequence of cloned cDNA coding for		SEQUENCE OF 36-302.	Yoshitake S., Funatsu G., Funatsu M.,	"Isolation and sequences of peptic peptides,	Adric Biol Chem	[5]		Funatsu G., Kimura M., Funatsu M.;	"Primary structure of Ala chain of ricin				Kimura Y., Kusuoku H., Tada M., Takag	"Structural analyses of sugar chains					Weaver R.F.; "Genomic cloning and characterization of a ricin gene from Ricinus Gommunis."; "Nucleic Acids Res. 13:8019-8033(1985). [12] Nucleic Acids Res. 13:8019-8033(1985). [13] Rucleic Acids Res. 13:8019-8033(1985). SEQUENCE FROM N.A. MEDLINE=92163016; PubMed=1371405; Tregear J.M., Roberts L.M.; Tregear J.M., Roberts L.M.; Tregear J.M., Roberts L.M.; Tregear J.M., Roberts L.M.; Tregear J.M., Roberts L.M.; Income and three lectin pseudogenes."; SEQUENCE OF 12-576 FROM N.A. MEDLINE=8119479; PubMed=1838723; Lamb A., Roberts L.M., Lord J.M.; "Nucleotide sequence of cloned of DNA coding for preproricin."; [4] SEQUENCE OF 36-302. Yoshitake S., Funatsu G., Funatsu M.; Isolation and sequences of peptic peptides, and the complete Agric. Biol. Chem. 42:1267-1274(1978). [5] Funatsu G., Kimura M., Funatsu M.; "Primary structure of Ala chain of ricin D."; Agric. Biol. Chem. 43:221-2224(1979). [6] CARBOHYDRAIE-LINKAGE SITES, AND PARTIAL SEQUENCE. MEDLINE=90344223; PubMed=186851; Kimura Y., Kusuoku H., Takagi S., Funatsu G.; "Structural analyses of sugar chains from ricin A-chain variant."; Agric. Biol. Chem. 54:157-162(1990). REVIEW.
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Weston S.A., Tucker A.D., Thatcher D.R., Derbyshire D.J., Pauptit R.A.;
                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215
                                                                                                                                                                                                                                                                                                                                                                   "Structure-based identification of a ricin inhibitor."; J. Mol. Biol. 266:1043-1049(1997).
                                                                                                                                                                     "Structure of ricin B-chain at 2.5-A resolution."; Proteins 10:260-269(1991).
                                                                                      K-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF B-CHAIN.
                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF A-CHAIN.
MEDLINE=95082010; Pubmed=7990130;
                                                                                              MEDLINE=91352004; PubMed=1881881;
Katzin B.J., Collins E.J., Robertus J.D.;
"Structure of ricin A-chain at 2.5 A.";
Proteins 10:251-259(1991).
                         K-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
                                                                                                                                                   MEDLINE=91352005; Pubmed=1881882;
Rutenber E., Robertus J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93165632; PubMed=1287657;
                                                                                                                                                                                                                                                                                                                Biochemistry 35:11098-11103(1996)
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"Ricin.";
Foxicon 39:1723-1728(2001).
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INTERCHAIN
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InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
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PDB; 2AAI; 31-JAN-94.
PDB; IAPG; 31-JAN-94.
PDB; IFMP; 31-OCT-93.
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11L4; 16-JAN-02.
11L9; 16-JAN-02.
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Kin Y., Robertus J.D.;

"Analysis of several key active site residues of ricin A chain by mutagenesis and X-ray crystallography.";

"L protein Eng. 5:775-779(1992).

"I protein Eng. 5:775-779(1992).

"I responsible for inhibiting protein synthesis through the catalytic inactivation of 608 ribosomal subunits. It acts as a glycosidase that removes a specific adenine residue from an exposed loop of 288 ribosomal SNA. As this loop is involved in the binding of elongation factors, the modified ribosomes are unable to support protein synthesis. The A chain can inactivate a few thousand ribosomes compart in the binding of elongation synthesis. The A chain can inactivate a few thousand ribosomes compart in the binding of elongation make new once. A single A-chain molecule can therefore kill an animal cell. The B chain binds to cell receptors and facilitates the entry into the cell of the A chain, B chains are also responsible content in an intervance of the in
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-!- SUBUNIT: Disulfide-linked dimer of A and B chains.
-!- DOMAIN: The B chain is composed of two domains, each domain consists of 3 homologous subdomains (alpha, beta, gamma).
-!- PTM: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND THE MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY: TYPE 2 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "X-ray structure of recombinant ricin A-chain at 1.8-A resolution.";
                                                                      MEDLINE=87165983; PubMed=3558397;
Monfort W., Villafranca J.E., Monzingo A.F., Ernst S.R., Katzin B., Rutenber E., Xuong N.H., Hamlin R., Robertus J.D.;
"The three-dimensional structure of ricin at 2.8 A.";
J. Biol. Chem. 262:5398-5403(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Structure and activity of an active site substitution of ricin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF A-CHAIN.
MEDLINE-97240820; PubMed-9086280;
Yan X., Hollis T., Svinth M., Day P., Monzingo A.F., Milne G.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96374222; PubMed=8780513;
Day P.J., Ernst S.R., Frankel A.E., Monzingo A.F., Pascal J.M.,
Molina-Svinth M.C., Robertus J.D.;
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SIMILARITY: Contains 2 ricin B-type lectin domains.
CAUTION: REF.4 AND REF.5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS
WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50231; RICIN B LECTIN; 2.
PROSITE; PS00275; SHIGA_RICIN; 1.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Signal; 3D-structure.
1 35.
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N-LINKED [GLCNAC. . .) (IN MINOR FORM).
/FTIG=CAR_000081.
N-LINKED [GLCNAC. . .).
N-LINKED [GLCNAC. . .).
N-LINKED [GLCNAC. . .).
                                                                                                                                     NOTE-Issue 31 of February 2003;
WWW="http://www.expasy.org/spotlight/articles/sptlt031.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .).
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RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
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-> R (IN REF. 3).
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LINKER PEPTIDE.
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                                                                      1;
                                                                                                                                                                                                                                              SNHAELSVILALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 112
                                                                                                                                                                                                                                                                                                        98 SNHAELSVTLALDVTNAYVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGN 157
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Lin T.T.-S., Li S.S.-Li;
Lin T.T.-S., Li S.S.-Li;
Lin T.T.-S., Li S.S.-Li;
Lin T.T.-S., Li S.S.-Li;
Lin T.T.-S., Li S.S.-Li;
Lin T.T.-S., Li S.S.-Li;
Lin T.T.-S., Li S.S.-Li;
Lin Strication and physicochemical properties of ricins and agglutinins from Ricinus communis.";
Lochem. 105:453-459(1980).
Lochem. 105:453-459(1980).
Lochem. 105:453-459(1980).
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Lochem. 105:
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                                                                                                                                -----VLPNRVGLPINORFILVEL
                                                                                                                                                                                    38 PKOYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVEL
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MEDLINE=86059449; PubMed=2999130;
Roberts L.M., Lamb F.I., Pappin D.J.C., Lord J.M.;
"The primary sequence of Ricinus communis agglutinin. Comparison with ricin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota: Viridiplantae; Szar, Smbryophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
                                                                      Gaps
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"The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin isolated from large-grain castor bean seeds."; Biochim. Biophys. Acta 872:277-285(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
20-FEB-2003 (Rel. 41, Last annotation update)
Agglutinin precursor (RCA) [Contains: Agglutinin A chain (rRNA N-glycosidase) (EC 3.2.2.2); Agglutinin B chain).
Ricinus communis (Castor bean).
                                                                      10;
   97.5%; Score 941; DB 1; Length 576; 94.9%; Pred. No. 1.5e-79; ive 0; Mismatches 0; Indels
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EMBL; S40368; AAB22584.1; -.
                                                                Conservative
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                                   Similarity
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Query Match
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YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 172
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                                                                                                                      PRINTS; PR00396; SHIGARICIN.
SMART; SM004396; SHIGARICIN.
PROSITE; PS50231; RICIN B LECTIN; 2.
PROSITE; PS00275; SHIGA_RICIN; 1.
PLANT defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; Glycoprotein; Lectin; Signal.

SIGNAL

1 24
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .).
N-LINKED (GLCNAC. . .).
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.8e-71;
ss 8; Indels 11;
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01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Klibosome-inactivating protein alpha-trichosanthin precursor (rRNA N-glycosidase) (EC 3.2.2.2) (Alpha-TCS).
Trichosanthes kirilowii (Mongolian snake-gourd).
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RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
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N -> D (IN REF. 2).

R -> G (IN REF. 2).

R -> T (IN REF. 2).

F -> V (IN REF. 2).

7. D455F2A72F609759 CF.
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LINKER PEPTIDE.
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Pred. No. 2.8
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2-ALPHA.
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                                      InterPro; Pro% Rough 18 lectin.
InterPro; IPR0007574; Ricin_B_lectin.
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF0061; RIP; T.
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86.7%;
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Matches 170; Conservative
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466
509
                   HSSP; P02879; IBR6.
GlycoSuiteDB; P06750;
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552
564 AA;
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MEDLINE=95344383; PubMed=75,030.
Menag Y., Liu S., Tang Y., Jin S., Wang Y.;

"Studies on crystal structures, active-centre geometry and deputinating mechanism of two ribosome-inactivating proteins.";

Biochem. J. 309:285-298(1995).
-!- FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. IT IS CAPABLE OF INHIBITING HIV-1 INFECTION AND REPLICATION. IT INACTIVATES EUKARYOTIC 608 RIBOSOMAL SHBUNITS.
-!- CAPABLE OF CATIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S FRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE I RIP SUBFAMILY.
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRALIP-MAXIMOWICZ; TISSUE=Leaf;
MEDLINE=90256790; PubMed=214400;
Chow T., Feldman R.A., Lovett M., Piatak M.;
"Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I ribosome-inactivating protein.";
J. Biol. Chem. 265:8670-8670-19990).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
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MEDLINE=90256789; PubMed=2341399;
Collins E.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.R.,
Wu P., Hwang K., Piatak M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Tuberous root;
Wang Y., Qian R.Q., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X.,
Tian G.Y., Ni C.Z.;
"Scientific evaluation of Tian Hua Fen (THF): history, chemistry and
Pure Appl. Chem. 58:789-798(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Primary amino acid sequence of alpha-trichosanthin and molecular models for abrin A-chain and alpha-trichosanthin."; J. Biol. Chem. 265:8665-8669(1990).
                                                                                                                   STRAIN-Maximowicz;
MRDLINE-9115-867; PubMed=1999291;
Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;
"Cloning of trichosanthin cDNA and its expression in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94344957; PubMed=8066085; Zhou F., Fu Z., Chen M., Lin Y., Pan K.; "Structure of trichosanthin at 1.88-A resolution."; Proteins 19:4-13(1994).
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EMBL; J05434; AAA34206.1; -.
PIR; JT0566; RLTZT.
                                                                                                                                                                                                                      Gene 97:267-272(1991).
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                                                                                                   SEQUENCE FROM N.A.
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NCBI_TaxID=3677;
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Gaps
PDB; 1NLI; 21-JAN-03.
PDB; 1QD2; 24-APR-00.
InterPro; 1PR001574; RIP.
Pfan; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA RICIN; 1.
PROSITE; PALIVITAI; Protein synthesis inhibitor; Hydrolase;
                                                           RIBOSOME-INACTIVATING PROTEIN ALPHA-
TRICHOSANTHIN.
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| MISSING (IN REF. 4). |
| -> L (IN REF. 4). |
| V -> VUAGLERNAVL (IN REF. 4). |
| KI -> GL (IN REF. 4). |
| K -> S (IN REF. 4). |
| K -> S (IN REF. 4). |
| WS -> LWL (IN REF. 4). |
| WS -> LWL (IN REF. 4). |
| WS -> T (IN REF. 4). |
| C -> T (IN REF. 2). |
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| MISSING (IN REF. 2). |
| MISSING (IN REF. 2). |
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                                                                         MISSING IN MATURE PROTEIN BY SIMILARITY.
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                                              Coxin; Signal; 3D-structure.
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Matches 72; Conservative
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1MRJ; 07-FEB-95. 1MRK; 07-FEB-95. 1TCS; 10-JUL-95. 1J4G; 28-JAN-03.

PDB; PDB; PDB;

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MEDINBE-1266957; PubMed=2050149;

REDINBE-1266957; PubMed=2050149;

REDINBE-1266957; PubMed=2050149;

REDINBERGABLIN: Genomic cloning, characterisation and the expression of the A-chain in Escherichia coli.";

ELL. J. Biochem. 198:723-732(1991).

CC SYNTHESIS THROUGH THE CATALITIC INACTIVATION OF 608 FINDSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S.RNA. THE CC BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.

CC BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.

CC COTALITIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 288 rkNA.

CC -- SUBUNIT: DISULFIDE-LINKED DIMER OF AND B CHAINS.

CC -- SUBUNIT: DISULFIDE-LINKED DIMER OF TWO DOMAINS. EACH DOMAIN CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).

CC -- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-CC INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.

CC -- SIMILARITY: CONTAINS 2 ricin B-type lectin domains.
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                                                                                                                                                                                                                                                   QLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 177
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                                                                      01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 41, Last amnotation update)
02-SPEB-2003 (Rel. 41, Last amnotation update)
03-SPEB-2013 (Greative Contains: Abrin-c A chain (rRNA N-glycosidase)
03-SPE (EC 3.2.2.2); Abrin-c B chain]
04-Creative Tradian licorice) (Crab's eye).
05-Creative Tracheophyta; Streptophyta; Euchryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; Creative Creat
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SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN B LECTIN; 2.
PROSITE; PS00275; SHIGA RICIN; 1.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
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95 RESIEVGIDVINAYVAYRAGSQSYFL---RDAPASASTYLFPGTQ-RYSLRFDGSYGDL
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I; Cucurbitales; Cucurbitaceae, Trichosanthes.
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ABRIN C A CHAIN (BY SIMILARITY)
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15-DEC-1998 (Rel. 37, Last sequence update)
28-FBE-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein karasurin precursor (rRNA N-91ycosidase) (BC 3.2.2.2)
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43.9%; Pred. No. 8.9e-23;
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Biol. Pharm. Bull. 20:711-713(1997).
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